

55063

Delaval, Jan

From: Huynh, Phuong N.
Sent: Monday, November 19, 2001 8:12 AM
To: Delaval, Jan
Subject: RE: 09/610,118

Good morning Jan!

Please search polypeptide of SEQ ID NO: 66, 61, 62, 63, 64, 65 against commercial and interference databases.

Thank you ☺

Neon
Art unit 1644
Mail CM1, 9E12
Office CM1, 9D06
Tel 308-4844

264
132
132

Point of Contact:
Jan Delaval
Librarian-Physical Sciences
CM1 1E01 Tel: 308-4498

THIS PAGE BLANK (USPTO)

Access DB#

55063

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Point of Contact:

Jan Delaval

Librarian-Physical Sciences

CM1 1E01 Tel: 308-4498

STAFF USE ONLY**Type of Search****Vendors and cost where applicable**

Searcher: Jan NA Sequence (#) _____ STN _____
 Searcher Phone #: 498 AA Sequence (#) 6 Dialog _____
 Searcher Location: _____ Structure (#) _____ Questel/Orbit _____
 Date Searcher Picked Up: 11/19 Bibliographic 1 Dr. Link _____
 Date Completed: 11/19 Litigation _____ Lexis/Nexis _____
 Searcher Prep & Review Time: _____ Fulltext _____ Sequence Systems ✓
 Clerical Prep Time: 25 Patent Family _____ WWW/Internet _____
 Online Time: +15 Other _____ Other (specify) _____

PTO-1590 (8-01)

THIS PAGE BLANK (USPTO)

GenCode version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 19, 2001, 08:11:07 ; Search time 48.99 Seconds
7.775 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: PIR:681*
2: PIR:21*
3: PIR:3*
4: PIR:4*

Pred. No. is the number of results predicted by chance to have a score greater than the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	98	P10123	Ig heavy chain V-1
2	31	100.0	101	S26450	Ig heavy chain V-1
3	31	100.0	110	PH1655	Ig heavy chain V-1
4	31	100.0	114	S36280	Ig heavy chain V-1
5	31	100.0	115	S36714	Ig heavy chain V-1
6	31	100.0	117	S17078	Ig heavy chain V-1
7	31	100.0	118	S00700	Ig heavy chain V-1
8	31	100.0	122	A33989	Ig heavy chain V-1
9	31	100.0	122	S31675	Ig heavy chain V-1
10	31	100.0	136	S31587	Ig heavy chain V-1
11	31	100.0	139	S13788	Ig heavy chain V-1
12	31	100.0	142	B84459	Ig heavy chain V-1
13	31	100.0	142	B84459	Ig heavy chain V-1
14	31	100.0	154	A32686	Ig heavy chain V-1
15	31	100.0	154	A32686	Ig heavy chain V-1
16	31	100.0	154	A32686	Ig heavy chain V-1
17	31	100.0	154	A32686	Ig heavy chain V-1
18	31	100.0	154	A32686	Ig heavy chain V-1
19	31	100.0	154	A32686	Ig heavy chain V-1
20	31	100.0	154	A32686	Ig heavy chain V-1
21	31	100.0	154	A32686	Ig heavy chain V-1
22	31	100.0	154	A32686	Ig heavy chain V-1
23	31	100.0	154	A32686	Ig heavy chain V-1
24	31	100.0	154	A32686	Ig heavy chain V-1
25	31	100.0	154	A32686	Ig heavy chain V-1
26	31	100.0	154	A32686	Ig heavy chain V-1
27	31	100.0	154	A32686	Ig heavy chain V-1
28	31	100.0	154	A32686	Ig heavy chain V-1
29	31	100.0	154	A32686	Ig heavy chain V-1
30	31	100.0	154	A32686	Ig heavy chain V-1

ALIGNMENTS

30	28	90.3	190	2	A54318	22.6k segment ant
31	28	90.3	181	2	S82158	gene s122 protein
32	28	90.3	216	2	A72281	conserved hypotet
33	28	90.3	220	2	A69736	hypothetical prote
34	28	90.3	226	2	T29404	hypothetical prote
35	28	90.3	246	2	I48302	collagen alpha 5(I
36	28	90.3	253	2	I48304	collagen alpha 5(I
37	28	90.3	253	2	I48304	collagen alpha 1(I
38	28	90.3	253	2	B83538	collagen alpha 1(I
39	28	90.3	253	2	A34476	collagen alpha 1(I
40	28	90.3	309	2	S43575	collagen alpha 4(I
41	28	90.3	312	2	I48303	collagen alpha 4(I
42	28	90.3	342	2	A85635	part of regulat
43	28	90.3	342	2	A85635	periplasmic protei
44	28	90.3	349	2	C82427	
45	28	90.3	349	2	C82427	

RESULT 1

P10123

Ig heavy chain V-III region (TD-VI) - human (fragment)

C:Species: Homo sapiens (human)

C:Accession: P10123; S26897

R:Bird, J.; Gallil, N.; Link, M.; Stiles, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobu

A:Reference number: P10116; MIM:682603

A:Accession: S26897

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: MIM:612154; MIM:612930; PIDN:CA78224.1; PID:932391

A:Notes: The sequences shows the V region (TD-VI) from a hyperactive DNA rearrangement

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 777-788, 1990

A:Reference number: S26885; MIM:93021117

A:Accession: S26897

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: MIM:612154; MIM:612930; PIDN:CA78224.1; PID:932391

A:Notes: The sequences shows the V region (TD-VI) from a hyperactive DNA rearrangement

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 777-788, 1990

A:Reference number: S26885; MIM:93021117

A:Accession: S26897

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: MIM:612154; MIM:612930; PIDN:CA78224.1; PID:932391

A:Notes: The sequences shows the V region (TD-VI) from a hyperactive DNA rearrangement

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 777-788, 1990

A:Reference number: S26885; MIM:93021117

A:Accession: S26897

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: MIM:612154; MIM:612930; PIDN:CA78224.1; PID:932391

A:Notes: The sequences shows the V region (TD-VI) from a hyperactive DNA rearrangement

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 777-788, 1990

A:Reference number: S26885; MIM:93021117

A:Accession: S26897

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <KAV>
 A:Cross-references: EMBL:X59106; NID:951707; PIRN:CA41832.1; PIR:951708
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin

Query Match
 Best Local Similarity 100.0%; Score 31; DB 2; Length 101;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SYNWS 5
 Db 13 SYNWS 17

RESULT 3
 I9 heavy chain V region (clone 288) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: P1655
 R:Clustal: J.L.; Kerr, N.S.; Opplinger, I.R.; Manlik, M.; Sasso, E.H.
 A:Title: Med. 118, 331-336, 1993
 A:Abstract: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A is discussed.
 A:Reference number: P1655
 A:Accession: P1655
 A:Molecule type: mRNA
 A:Residues: 1-110 <HTL>
 A:Experimental source: B cell
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:7-90/Domain: Immunoglobulin homology <IMW>

Query Match
 Best Local Similarity 100.0%; Score 31; DB 2; Length 110;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SYNWS 5
 Db 23 SYNWS 27

RESULT 4
 I9 heavy chain V region (clone alpha-FOC-43) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
 R:Clustal: S35280
 EMBL J:12, 725-734
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.
 A:Reference number: S35280; M01D:9317846
 A:Accession: S35280
 A:Molecule type: mRNA
 A:Experimental source: B cell
 A:Residues: 1-114 <SVT>
 A:Cross-references: EMBL:X18832
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: Immunoglobulin homology <IMW>

Query Match
 Best Local Similarity 100.0%; Score 31; DB 2; Length 114;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SYNWS 5
 Db 31 SYNWS 35

RESULT 5 -

S38714
 I9 heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
 R:Clustal: S38714
 submitted to the EMBL Data Library, November 1993

Query Match
 Best Local Similarity 100.0%; Score 31; DB 2; Length 115;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SYNWS 5
 Db 30 SYNWS 34

RESULT 6
 I9 heavy chain V region (clone FLJ3-28) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 10-May-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
 C:Accession: S78486; S31115
 R:Rappoport, F.M.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S78486
 A:Accession: S78486
 A:Molecule type: mRNA
 A:Experimental source: B cell
 A:Residues: 1-117 <KAV>
 A:Cross-references: EMBL:X62965
 A:Experimental source: clone FLJ3-28
 R:Rappoport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.N.; Schuur
 Eur. J. Immunol. 22, 247-251, 1992
 A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
 A:Accession: S31115
 A:Molecule type: mRNA
 A:Residues: 1-4, 'L', '6', '32', '6', '34-52', 'E', '54-73', 'K', '75-97 <KAV>
 A:Cross-references: EMBL:X62965
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: Immunoglobulin homology <IMW>

Query Match
 Best Local Similarity 100.0%; Score 31; DB 2; Length 117;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SYNWS 5
 Db 31 SYNWS 35

RESULT 7
 I9 heavy chain V-gene (clone HHC19) - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S60299; S17079
 R:Knapperts, R.; Fischer, U.; Rejovsky, K.; Gause, A.
 Immunol. Rev. 34, 57-62, 1992
 A:Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive
 A:Reference number: S60299; M01D:9312853

A:Accession: S60299
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <NU>
 A:Cross-references: EMBL:652128; NID:938340; PIDD:CA44059.1; PIDD:938341
 A:Cross-references: authors did not translate the codons for residues 6, 52, 54, 68, 69, 71, 72.
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:34-117/Domain: Immunoglobulin homology <IM>

Query Match 100.0%; Score 31; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYNMS 5
 DB 50 SYNMS 54

RESULT 8
 S00700
 19 heavy chain V region - African clawed frog
 C:Accession: S00700
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
 R:Yamawaki-Kataoka, Y.; Honjo, T.
 Nucleic Acids Res. 15, 5888, 1987
 A:Title: Nucleotide sequence of the variable region segments of the immunoglobulin heavy chain of the African clawed frog (Xenopus laevis).
 A:Reference number: S00700; NID:87289054
 A:Accession: S00700
 A:Molecule type: DNA
 A:Residues: 1-118 <YAN>
 A:Cross-references: EMBL:Y00380; NID:964810; PIDD:CA468452.1; PIDD:964811
 A:Note: the sequence was determined from the germline gene
 C:Genetics:
 A:Introns: 15/3
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:34-117/Domain: Immunoglobulin homology <IM>

Query Match 100.0%; Score 31; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYNMS 5
 DB 50 SYNMS 54

RESULT 9
 A33989
 19 heavy chain V-1-D-J region - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)1990 #text_change 16-Aug-1996
 C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990
 C:Accession: A33989
 R:Chen, J. J.; Alt, F. W.
 Proc. Natl. Acad. Sci. U.S.A. 86, 8010-8014, 1989
 A:Title: Evolution of immunoglobulin genes: V-H families in the amphibian Xenopus.
 A:Reference number: A33989; NID:90046727
 A:Accession: A33989
 A:Status: preliminary; not compared with conceptual translation
 A:Introns: 15/3
 A:Residues: 1-122 <RSU>
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:15-100/Domain: Immunoglobulin homology <IM>

Query Match 100.0%; Score 31; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYNMS 5
 DB 31 SYNMS 35

RESULT 10
 S31675
 19 heavy chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1992 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31675
 R:Gaultier, L.; Bouhili, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
 A:Reference number: S31585
 A:Accession: S31675
 A:Status: preliminary
 A:Introns: 15/3
 A:Residues: 1-122 <CU>
 A:Cross-references: EMBL:Z14175; NID:931015; PIDD:CA478544.1; PIDD:931016
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:21-104/Domain: Immunoglobulin homology <IM>

Query Match 100.0%; Score 31; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYNMS 5
 DB 37 SYNMS 41

RESULT 11
 S31587
 19 heavy chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31587
 R:Cuisinier, A. M.; Gaultier, L.; Bouhili, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
 A:Reference number: S31585
 A:Accession: S31587
 A:Status: preliminary
 A:Introns: 15/3
 A:Residues: 1-136 <CU>
 A:Cross-references: EMBL:Z14189; NID:931005; PIDD:CA478558.1; PIDD:931006
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:31-119/Domain: Immunoglobulin homology <IM>

Query Match 100.0%; Score 31; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYNMS 5
 DB 47 SYNMS 51

RESULT 12
 S25475
 19 variable region (VDJ) (clone 721-9) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
 C:Accession: S25475
 R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:13:32 : Search time 27.32 Seconds
(without alignments)
6.269 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYMS 5

Scoring table: BLOSUMP2
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	DB	ID	Description
1	31	100.0	1254	1	DPROG_YEAST	P15801 saccharomyces
2	28	90.3	180	1	ORNL_SCHPO	O14525 schizosacch
3	28	90.3	190	1	TREO_SCHMA	P34922 caenorhabd
4	28	90.3	342	1	TORT_ECOLI	P36863 escherichia
5	28	90.3	359	1	DNLI_BPTT	P00566 bacterioph
6	28	90.3	385	1	YMBM_BACSD	P39396 bacillus su
7	28	90.3	393	1	Y306_MYCE	P37348 mycoplasma
8	28	90.3	455	1	YAO6_AYCHO	O10085 schizosacch
9	28	90.3	451	1	CA04_PROVIN	O14525 schizosacch
10	28	90.3	593	1	PHMC_PACA	O14525 schizosacch
11	28	90.3	754	1	CA54_CANRA	O68317 calanus norv
12	28	90.3	754	1	CA54_CANRA	O68317 calanus norv
13	28	90.3	1669	1	CA14_HUMAN	P02462 homo sapien
14	28	90.3	1669	1	CA14_HUMAN	P02462 homo sapien
15	28	90.3	1670	1	CA14_HUMAN	P02462 homo sapien
16	28	90.3	1670	1	CA14_HUMAN	P02462 homo sapien
17	28	90.3	1670	1	CA14_HUMAN	P02462 homo sapien
18	28	90.3	1670	1	CA14_HUMAN	P02462 homo sapien
19	28	90.3	1670	1	CA14_HUMAN	P02462 homo sapien
20	28	90.3	1670	1	CA14_HUMAN	P02462 homo sapien
21	28	90.3	1758	1	CA24_HUMAN	P08572 homo sapien
22	28	90.3	1758	1	CA24_HUMAN	P08572 homo sapien
23	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
24	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
25	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
26	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
27	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
28	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
29	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
30	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
31	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
32	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd
33	28	90.3	2210	1	RHPL_EBOSH	P17140 caenorhabd

34	27	87.1	117	1	HV42_MOUSE	P01812 mus muscu
35	27	87.1	117	1	HV49_MOUSE	P06328 mus muscu
36	27	87.1	118	1	HV39_MOUSE	P01807 mus muscu
37	27	87.1	119	1	HV38_MOUSE	P01808 mus muscu
38	27	87.1	119	1	HV40_MOUSE	P01810 mus muscu
39	27	87.1	120	1	HV07_MOUSE	P06329 mus muscu
40	27	87.1	139	1	HV07_MOUSE	P01751 mus muscu
41	27	87.1	173	1	NUGM_LATOH	O03175 latimeria c
42	27	87.1	355	1	PRYC_SLUNG	O02360 dirosophis
43	27	87.1	355	1	F02_DROME	P16482 klebsiella
44	27	87.1	444	1	CITL_ALERN	
45	27	87.1	444	1	CITL_ALERN	

ALIGNMENTS

```

RESULT 1
ID DPROG_YEAST STANDARD; PRT; 1254 AA.
DI 1 DPROG_YEAST
DI 2 DPROG_YEAST
DI 3 DPROG_YEAST
DI 4 DPROG_YEAST
DI 5 DPROG_YEAST
DI 6 DPROG_YEAST
DI 7 DPROG_YEAST
DI 8 DPROG_YEAST
DI 9 DPROG_YEAST
DI 10 DPROG_YEAST
DI 11 DPROG_YEAST
DI 12 DPROG_YEAST
DI 13 DPROG_YEAST
DI 14 DPROG_YEAST
DI 15 DPROG_YEAST
DI 16 DPROG_YEAST
DI 17 DPROG_YEAST
DI 18 DPROG_YEAST
DI 19 DPROG_YEAST
DI 20 DPROG_YEAST
DI 21 DPROG_YEAST
DI 22 DPROG_YEAST
DI 23 DPROG_YEAST
DI 24 DPROG_YEAST
DI 25 DPROG_YEAST
DI 26 DPROG_YEAST
DI 27 DPROG_YEAST
DI 28 DPROG_YEAST
DI 29 DPROG_YEAST
DI 30 DPROG_YEAST
DI 31 DPROG_YEAST
DI 32 DPROG_YEAST
DI 33 DPROG_YEAST
DI 34 DPROG_YEAST
DI 35 DPROG_YEAST
DI 36 DPROG_YEAST
DI 37 DPROG_YEAST
DI 38 DPROG_YEAST
DI 39 DPROG_YEAST
DI 40 DPROG_YEAST
DI 41 DPROG_YEAST
DI 42 DPROG_YEAST
DI 43 DPROG_YEAST
DI 44 DPROG_YEAST
DI 45 DPROG_YEAST
DI 46 DPROG_YEAST
DI 47 DPROG_YEAST
DI 48 DPROG_YEAST
DI 49 DPROG_YEAST
DI 50 DPROG_YEAST
DI 51 DPROG_YEAST
DI 52 DPROG_YEAST
DI 53 DPROG_YEAST
DI 54 DPROG_YEAST
DI 55 DPROG_YEAST
DI 56 DPROG_YEAST
DI 57 DPROG_YEAST
DI 58 DPROG_YEAST
DI 59 DPROG_YEAST
DI 60 DPROG_YEAST
DI 61 DPROG_YEAST
DI 62 DPROG_YEAST
DI 63 DPROG_YEAST
DI 64 DPROG_YEAST
DI 65 DPROG_YEAST
DI 66 DPROG_YEAST
DI 67 DPROG_YEAST
DI 68 DPROG_YEAST
DI 69 DPROG_YEAST
DI 70 DPROG_YEAST
DI 71 DPROG_YEAST
DI 72 DPROG_YEAST
DI 73 DPROG_YEAST
DI 74 DPROG_YEAST
DI 75 DPROG_YEAST
DI 76 DPROG_YEAST
DI 77 DPROG_YEAST
DI 78 DPROG_YEAST
DI 79 DPROG_YEAST
DI 80 DPROG_YEAST
DI 81 DPROG_YEAST
DI 82 DPROG_YEAST
DI 83 DPROG_YEAST
DI 84 DPROG_YEAST
DI 85 DPROG_YEAST
DI 86 DPROG_YEAST
DI 87 DPROG_YEAST
DI 88 DPROG_YEAST
DI 89 DPROG_YEAST
DI 90 DPROG_YEAST
DI 91 DPROG_YEAST
DI 92 DPROG_YEAST
DI 93 DPROG_YEAST
DI 94 DPROG_YEAST
DI 95 DPROG_YEAST
DI 96 DPROG_YEAST
DI 97 DPROG_YEAST
DI 98 DPROG_YEAST
DI 99 DPROG_YEAST
DI 100 DPROG_YEAST
DI 101 DPROG_YEAST
DI 102 DPROG_YEAST
DI 103 DPROG_YEAST
DI 104 DPROG_YEAST
DI 105 DPROG_YEAST
DI 106 DPROG_YEAST
DI 107 DPROG_YEAST
DI 108 DPROG_YEAST
DI 109 DPROG_YEAST
DI 110 DPROG_YEAST
DI 111 DPROG_YEAST
DI 112 DPROG_YEAST
DI 113 DPROG_YEAST
DI 114 DPROG_YEAST
DI 115 DPROG_YEAST
DI 116 DPROG_YEAST
DI 117 DPROG_YEAST
DI 118 DPROG_YEAST
DI 119 DPROG_YEAST
DI 120 DPROG_YEAST
DI 121 DPROG_YEAST
DI 122 DPROG_YEAST
DI 123 DPROG_YEAST
DI 124 DPROG_YEAST
DI 125 DPROG_YEAST
DI 126 DPROG_YEAST
DI 127 DPROG_YEAST
DI 128 DPROG_YEAST
DI 129 DPROG_YEAST
DI 130 DPROG_YEAST
DI 131 DPROG_YEAST
DI 132 DPROG_YEAST
DI 133 DPROG_YEAST
DI 134 DPROG_YEAST
DI 135 DPROG_YEAST
DI 136 DPROG_YEAST
DI 137 DPROG_YEAST
DI 138 DPROG_YEAST
DI 139 DPROG_YEAST
DI 140 DPROG_YEAST
DI 141 DPROG_YEAST
DI 142 DPROG_YEAST
DI 143 DPROG_YEAST
DI 144 DPROG_YEAST
DI 145 DPROG_YEAST
DI 146 DPROG_YEAST
DI 147 DPROG_YEAST
DI 148 DPROG_YEAST
DI 149 DPROG_YEAST
DI 150 DPROG_YEAST
DI 151 DPROG_YEAST
DI 152 DPROG_YEAST
DI 153 DPROG_YEAST
DI 154 DPROG_YEAST
DI 155 DPROG_YEAST
DI 156 DPROG_YEAST
DI 157 DPROG_YEAST
DI 158 DPROG_YEAST
DI 159 DPROG_YEAST
DI 160 DPROG_YEAST
DI 161 DPROG_YEAST
DI 162 DPROG_YEAST
DI 163 DPROG_YEAST
DI 164 DPROG_YEAST
DI 165 DPROG_YEAST
DI 166 DPROG_YEAST
DI 167 DPROG_YEAST
DI 168 DPROG_YEAST
DI 169 DPROG_YEAST
DI 170 DPROG_YEAST
DI 171 DPROG_YEAST
DI 172 DPROG_YEAST
DI 173 DPROG_YEAST
DI 174 DPROG_YEAST
DI 175 DPROG_YEAST
DI 176 DPROG_YEAST
DI 177 DPROG_YEAST
DI 178 DPROG_YEAST
DI 179 DPROG_YEAST
DI 180 DPROG_YEAST
DI 181 DPROG_YEAST
DI 182 DPROG_YEAST
DI 183 DPROG_YEAST
DI 184 DPROG_YEAST
DI 185 DPROG_YEAST
DI 186 DPROG_YEAST
DI 187 DPROG_YEAST
DI 188 DPROG_YEAST
DI 189 DPROG_YEAST
DI 190 DPROG_YEAST
DI 191 DPROG_YEAST
DI 192 DPROG_YEAST
DI 193 DPROG_YEAST
DI 194 DPROG_YEAST
DI 195 DPROG_YEAST
DI 196 DPROG_YEAST
DI 197 DPROG_YEAST
DI 198 DPROG_YEAST
DI 199 DPROG_YEAST
DI 200 DPROG_YEAST
DI 201 DPROG_YEAST
DI 202 DPROG_YEAST
DI 203 DPROG_YEAST
DI 204 DPROG_YEAST
DI 205 DPROG_YEAST
DI 206 DPROG_YEAST
DI 207 DPROG_YEAST
DI 208 DPROG_YEAST
DI 209 DPROG_YEAST
DI 210 DPROG_YEAST
DI 211 DPROG_YEAST
DI 212 DPROG_YEAST
DI 213 DPROG_YEAST
DI 214 DPROG_YEAST
DI 215 DPROG_YEAST
DI 216 DPROG_YEAST
DI 217 DPROG_YEAST
DI 218 DPROG_YEAST
DI 219 DPROG_YEAST
DI 220 DPROG_YEAST
DI 221 DPROG_YEAST
DI 222 DPROG_YEAST
DI 223 DPROG_YEAST
DI 224 DPROG_YEAST
DI 225 DPROG_YEAST
DI 226 DPROG_YEAST
DI 227 DPROG_YEAST
DI 228 DPROG_YEAST
DI 229 DPROG_YEAST
DI 230 DPROG_YEAST
DI 231 DPROG_YEAST
DI 232 DPROG_YEAST
DI 233 DPROG_YEAST
DI 234 DPROG_YEAST
DI 235 DPROG_YEAST
DI 236 DPROG_YEAST
DI 237 DPROG_YEAST
DI 238 DPROG_YEAST
DI 239 DPROG_YEAST
DI 240 DPROG_YEAST
DI 241 DPROG_YEAST
DI 242 DPROG_YEAST
DI 243 DPROG_YEAST
DI 244 DPROG_YEAST
DI 245 DPROG_YEAST
DI 246 DPROG_YEAST
DI 247 DPROG_YEAST
DI 248 DPROG_YEAST
DI 249 DPROG_YEAST
DI 250 DPROG_YEAST
DI 251 DPROG_YEAST
DI 252 DPROG_YEAST
DI 253 DPROG_YEAST
DI 254 DPROG_YEAST
DI 255 DPROG_YEAST
DI 256 DPROG_YEAST
DI 257 DPROG_YEAST
DI 258 DPROG_YEAST
DI 259 DPROG_YEAST
DI 260 DPROG_YEAST
DI 261 DPROG_YEAST
DI 262 DPROG_YEAST
DI 263 DPROG_YEAST
DI 264 DPROG_YEAST
DI 265 DPROG_YEAST
DI 266 DPROG_YEAST
DI 267 DPROG_YEAST
DI 268 DPROG_YEAST
DI 269 DPROG_YEAST
DI 270 DPROG_YEAST
DI 271 DPROG_YEAST
DI 272 DPROG_YEAST
DI 273 DPROG_YEAST
DI 274 DPROG_YEAST
DI 275 DPROG_YEAST
DI 276 DPROG_YEAST
DI 277 DPROG_YEAST
DI 278 DPROG_YEAST
DI 279 DPROG_YEAST
DI 280 DPROG_YEAST
DI 281 DPROG_YEAST
DI 282 DPROG_YEAST
DI 283 DPROG_YEAST
DI 284 DPROG_YEAST
DI 285 DPROG_YEAST
DI 286 DPROG_YEAST
DI 287 DPROG_YEAST
DI 288 DPROG_YEAST
DI 289 DPROG_YEAST
DI 290 DPROG_YEAST
DI 291 DPROG_YEAST
DI 292 DPROG_YEAST
DI 293 DPROG_YEAST
DI 294 DPROG_YEAST
DI 295 DPROG_YEAST
DI 296 DPROG_YEAST
DI 297 DPROG_YEAST
DI 298 DPROG_YEAST
DI 299 DPROG_YEAST
DI 300 DPROG_YEAST
DI 301 DPROG_YEAST
DI 302 DPROG_YEAST
DI 303 DPROG_YEAST
DI 304 DPROG_YEAST
DI 305 DPROG_YEAST
DI 306 DPROG_YEAST
DI 307 DPROG_YEAST
DI 308 DPROG_YEAST
DI 309 DPROG_YEAST
DI 310 DPROG_YEAST
DI 311 DPROG_YEAST
DI 312 DPROG_YEAST
DI 313 DPROG_YEAST
DI 314 DPROG_YEAST
DI 315 DPROG_YEAST
DI 316 DPROG_YEAST
DI 317 DPROG_YEAST
DI 318 DPROG_YEAST
DI 319 DPROG_YEAST
DI 320 DPROG_YEAST
DI 321 DPROG_YEAST
DI 322 DPROG_YEAST
DI 323 DPROG_YEAST
DI 324 DPROG_YEAST
DI 325 DPROG_YEAST
DI 326 DPROG_YEAST
DI 327 DPROG_YEAST
DI 328 DPROG_YEAST
DI 329 DPROG_YEAST
DI 330 DPROG_YEAST
DI 331 DPROG_YEAST
DI 332 DPROG_YEAST
DI 333 DPROG_YEAST
DI 334 DPROG_YEAST
DI 335 DPROG_YEAST
DI 336 DPROG_YEAST
DI 337 DPROG_YEAST
DI 338 DPROG_YEAST
DI 339 DPROG_YEAST
DI 340 DPROG_YEAST
DI 341 DPROG_YEAST
DI 342 DPROG_YEAST
DI 343 DPROG_YEAST
DI 344 DPROG_YEAST
DI 345 DPROG_YEAST
DI 346 DPROG_YEAST
DI 347 DPROG_YEAST
DI 348 DPROG_YEAST
DI 349 DPROG_YEAST
DI 350 DPROG_YEAST
DI 351 DPROG_YEAST
DI 352 DPROG_YEAST
DI 353 DPROG_YEAST
DI 354 DPROG_YEAST
DI 355 DPROG_YEAST
DI 356 DPROG_YEAST
DI 357 DPROG_YEAST
DI 358 DPROG_YEAST
DI 359 DPROG_YEAST
DI 360 DPROG_YEAST
DI 361 DPROG_YEAST
DI 362 DPROG_YEAST
DI 363 DPROG_YEAST
DI 364 DPROG_YEAST
DI 365 DPROG_YEAST
DI 366 DPROG_YEAST
DI 367 DPROG_YEAST
DI 368 DPROG_YEAST
DI 369 DPROG_YEAST
DI 370 DPROG_YEAST
DI 371 DPROG_YEAST
DI 372 DPROG_YEAST
DI 373 DPROG_YEAST
DI 374 DPROG_YEAST
DI 375 DPROG_YEAST
DI 376 DPROG_YEAST
DI 377 DPROG_YEAST
DI 378 DPROG_YEAST
DI 379 DPROG_YEAST
DI 380 DPROG_YEAST
DI 381 DPROG_YEAST
DI 382 DPROG_YEAST
DI 383 DPROG_YEAST
DI 384 DPROG_YEAST
DI 385 DPROG_YEAST
DI 386 DPROG_YEAST
DI 387 DPROG_YEAST
DI 388 DPROG_YEAST
DI 389 DPROG_YEAST
DI 390 DPROG_YEAST
DI 391 DPROG_YEAST
DI 392 DPROG_YEAST
DI 393 DPROG_YEAST
DI 394 DPROG_YEAST
DI 395 DPROG_YEAST
DI 396 DPROG_YEAST
DI 397 DPROG_YEAST
DI 398 DPROG_YEAST
DI 399 DPROG_YEAST
DI 400 DPROG_YEAST
DI 401 DPROG_YEAST
DI 402 DPROG_YEAST
DI 403 DPROG_YEAST
DI 404 DPROG_YEAST
DI 405 DPROG_YEAST
DI 406 DPROG_YEAST
DI 407 DPROG_YEAST
DI 408 DPROG_YEAST
DI 409 DPROG_YEAST
DI 410 DPROG_YEAST
DI 411 DPROG_YEAST
DI 412 DPROG_YEAST
DI 413 DPROG_YEAST
DI 414 DPROG_YEAST
DI 415 DPROG_YEAST
DI 416 DPROG_YEAST
DI 417 DPROG_YEAST
DI 418 DPROG_YEAST
DI 419 DPROG_YEAST
DI 420 DPROG_YEAST
DI 421 DPROG_YEAST
DI 422 DPROG_YEAST
DI 423 DPROG_YEAST
DI 424 DPROG_YEAST
DI 425 DPROG_YEAST
DI 426 DPROG_YEAST
DI 427 DPROG_YEAST
DI 428 DPROG_YEAST
DI 429 DPROG_YEAST
DI 430 DPROG_YEAST
DI 431 DPROG_YEAST
DI 432 DPROG_YEAST
DI 433 DPROG_YEAST
DI 434 DPROG_YEAST
DI 435 DPROG_YEAST
DI 436 DPROG_YEAST
DI 437 DPROG_YEAST
DI 438 DPROG_YEAST
DI 439 DPROG_YEAST
DI 440 DPROG_YEAST
DI 441 DPROG_YEAST
DI 442 DPROG_YEAST
DI 443 DPROG_YEAST
DI 444 DPROG_YEAST
DI 445 DPROG_YEAST
DI 446 DPROG_YEAST
DI 447 DPROG_YEAST
DI 448 DPROG_YEAST
DI 449 DPROG_YEAST
DI 450 DPROG_YEAST
DI 451 DPROG_YEAST
DI 452 DPROG_YEAST
DI 453 DPROG_YEAST
DI 454 DPROG_YEAST
DI 455 DPROG_YEAST
DI 456 DPROG_YEAST
DI 457 DPROG_YEAST
DI 458 DPROG_YEAST
DI 459 DPROG_YEAST
DI 460 DPROG_YEAST
DI 461 DPROG_YEAST
DI 462 DPROG_YEAST
DI 463 DPROG_YEAST
DI 464 DPROG_YEAST
DI 465 DPROG_YEAST
DI 466 DPROG_YEAST
DI 467 DPROG_YEAST
DI 468 DPROG_YEAST
DI 469 DPROG_YEAST
DI 470 DPROG_YEAST
DI 471 DPROG_YEAST
DI 472 DPROG_YEAST
DI 473 DPROG_YEAST
DI 474 DPROG_YEAST
DI 475 DPROG_YEAST
DI 476 DPROG_YEAST
DI 477 DPROG_YEAST
DI 478 DPROG_YEAST
DI 479 DPROG_YEAST
DI 480 DPROG_YEAST
DI 481 DPROG_YEAST
DI 482 DPROG_YEAST
DI 483 DPROG_YEAST
DI 484 DPROG_YEAST
DI 485 DPROG_YEAST
DI 486 DPROG_YEAST
DI 487 DPROG_YEAST
DI 488 DPROG_YEAST
DI 489 DPROG_YEAST
DI 490 DPROG_YEAST
DI 491 DPROG_YEAST
DI 492 DPROG_YEAST
DI 493 DPROG_YEAST
DI 494 DPROG_YEAST
DI 495 DPROG_YEAST
DI 496 DPROG_YEAST
DI 497 DPROG_YEAST
DI 498 DPROG_YEAST
DI 499 DPROG_YEAST
DI 500 DPROG_YEAST
DI 501 DPROG_YEAST
DI 502 DPROG_YEAST
DI 503 DPROG_YEAST
DI 504 DPROG_YEAST
DI 505 DPROG_YEAST
DI 506 DPROG_YEAST
DI 507 DPROG_YEAST
DI 508 DPROG_YEAST
DI 509 DPROG_YEAST
DI 510 DPROG_YEAST
DI 511 DPROG_YEAST
DI 512 DPROG_YEAST
DI 513 DPROG_YEAST
DI 514 DPROG_YEAST
DI 515 DPROG_YEAST
DI 516 DPROG_YEAST
DI 517 DPROG_YEAST
DI 518 DPROG_YEAST
DI 519 DPROG_YEAST
DI 520 DPROG_YEAST
DI 521 DPROG_YEAST
DI 522 DPROG_YEAST
DI 523 DPROG_YEAST
DI 524 DPROG_YEAST
DI 525 DPROG_YEAST
DI 526 DPROG_YEAST
DI 527 DPROG_YEAST
DI 528 DPROG_YEAST
DI 529 DPROG_YEAST
DI 530 DPROG_YEAST
DI 531 DPROG_YEAST
DI 532 DPROG_YEAST
DI 533 DPROG_YEAST
DI 534 DPROG_YEAST
DI 535 DPROG_YEAST
DI 536 DPROG_YEAST
DI 537 DPROG_YEAST
DI 538 DPROG_YEAST
DI 539 DPROG_YEAST
DI 540 DPROG_YEAST
DI 541 DPROG_YEAST
DI 542 DPROG_YEAST
DI 543 DPROG_YEAST
DI 544 DPROG_YEAST
DI 545 DPROG_YEAST
DI 546 DPROG_YEAST
DI 547 DPROG_YEAST
DI 548 DPROG_YEAST
DI 549 DPROG_YEAST
DI 550 DPROG_YEAST
DI 551 DPROG_YEAST
DI 552 DPROG_YEAST
DI 553 DPROG_YEAST
DI 554 DPROG_YEAST
DI 555 DPROG_YEAST
DI 556 DPROG_YEAST
DI 557 DPROG_YEAST
DI 558 DPROG_YEAST
DI 559 DPROG_YEAST
DI 560 DPROG_YEAST
DI 561 DPROG_YEAST
DI 562 DPROG_YEAST
DI 563 DPROG_YEAST
DI 564 DPROG_YEAST
DI 565 DPROG_YEAST
DI 566 DPROG_YEAST
DI 567 DPROG_YEAST
DI 568 DPROG_YEAST
DI 569 DPROG_YEAST
DI 570 DPROG_YEAST
DI 571 DPROG_YEAST
DI 572 DPROG_YEAST
DI 573 DPROG_YEAST
DI 574 DPROG_YEAST
DI 575 DPROG_YEAST
DI 576 DPROG_YEAST
DI 577 DPROG_YEAST
DI 578 DPROG_YEAST
DI 579 DPROG_YEAST
DI 580 DPROG_YEAST
DI 581 DPROG_YEAST
DI 582 DPROG_YEAST
DI 583 DPROG_YEAST
DI 584 DPROG_YEAST
DI 585 DPROG_YEAST
DI 586 DPROG_YEAST
DI 587 DPROG_YEAST
DI 588 DPROG_YEAST
DI 589 DPROG_YEAST
DI 590 DPROG_YEAST
DI 591 DPROG_YEAST
DI 592 DPROG_YEAST
DI 593 DPROG_YEAST
DI 594 DPROG_YEAST
DI 595 DPROG_YEAST
DI 596 DPROG_YEAST
DI 597 DPROG_YEAST
DI 598 DPROG_YEAST
DI 599 DPROG_YEAST
DI 600 DPROG_YEAST
DI 601 DPROG_YEAST
DI 602 DPROG_YEAST
DI 603 DPROG_YEAST
DI 604 DPROG_YEAST
DI 605 DPROG_YEAST
DI 606 DPROG_YEAST
DI 607 DPROG_YEAST
DI 608 DPROG_YEAST
DI 609 DPROG_YEAST
DI 610 DPROG_YEAST
DI 611 DPROG_YEAST
DI 612 DPROG_YEAST
DI 613 DPROG_YEAST
DI 614 DPROG_YEAST
DI 615 DPROG_YEAST
DI 616 DPROG_YEAST
DI 617 DPROG_YEAST
DI 618 DPROG_YEAST
DI 619 DPROG_YEAST
DI 620 DPROG_YEAST
DI 621 DPROG_YEAST
DI 622 DPROG_YEAST
DI 623 DPROG_YEAST
DI 624 DPROG_YEAST
DI 625 DPROG_YEAST
DI 626 DPROG_YEAST
DI 627 DPROG_YEAST
DI 628 DPROG_YEAST
DI 629 DPROG_YEAST
DI 630 DPROG_YEAST
DI 631 DPROG_YEAST
DI 632 DPROG_YEAST
DI 633 DPROG_YEAST
DI 634 DPROG_YEAST
DI 635 DPROG_YEAST
DI 636 DPROG_YEAST
DI 637 DPROG_YEAST
DI 638 DPROG_YEAST
DI 639 DPROG_YEAST
DI 640 DPROG_YEAST
DI 641 DPROG_YEAST
DI 642 DPROG_YEAST
DI 643 DPROG_YEAST
DI 644 DPROG_YEAST
DI 645 DPROG_YEAST
DI 646 DPROG_YEAST
DI 647 DPROG_YEAST
DI 648 DPROG_YEAST
DI 649 DPROG_YEAST
DI 650 DPROG_YEAST
DI 651 DPROG_YEAST
DI 652 DPROG_YEAST
DI 653 DPROG_YEAST
DI 654 DPROG_YEAST
DI 655 DPROG_YEAST
DI 656 DPROG_YEAST
DI 657 DPROG_YEAST
DI 658 DPROG_YEAST
DI 659 DPROG_YEAST
DI 660 DPROG_YEAST
DI 661 DPROG_YEAST
DI 662 DPROG_YEAST
DI 663 DPROG_YEAST
DI 664 DPROG_YEAST
DI 665 DPROG_YEAST
DI 666 DPROG_YEAST
DI 667 DPROG_YEAST
DI 668 DPROG_YEAST
DI 669 DPROG_YEAST
DI 670 DPROG_YEAST
DI 671 DPROG_YEAST
DI 672 DPROG_YEAST
DI 673 DPROG_YEAST
DI 674 DPROG_YEAST
DI 675 DPROG_YEAST
DI 676 DPROG_YEAST
DI 677 DPROG_YEAST
DI 678 DPROG_YEAST
DI 679 DPROG_YEAST
DI 680 DPROG_YEAST
DI 681 DPROG_YEAST
DI 682 DPROG_YEAST
DI 683 DPROG_YEAST
DI 684 DPROG_YEAST
DI 685 DPROG_YEAST
DI 686 DPROG_YEAST
DI 687 DPROG_YEAST
DI 688 DPROG_YEAST
DI 689 DPROG_YEAST
DI 690 DPROG_YEAST
DI 691 DPRO
```


CC T7-like phages.
 CC DBL_TaxID=10760;
 RA MEDLINE=83241725; PubMed=6664790;
 RX Dunn J.J., Studier F.W.;
 RT Complete nucleotide sequence of bacteriophage T7 DNA and the
 RT locations of T7 genetic elements.*
 RT Mol. Biol. 166:477-535(1983).
 CC
 CC SEQUENCE FROM N.A.
 RA MEDLINE=82078034; PubMed=7310871;
 RX Dunn J.J., Studier F.W.;
 RT Nucleotide sequence from the genetic left end of bacteriophage T7
 RT DNA to the beginning of gene 4.*
 RT Mol. Biol. 148:303-340(1991).
 CC
 CC SEQUENCE OF 278-359 FROM N.A.
 RA MEDLINE=81053683; PubMed=7001354;
 RX Dunn J.J., Studier F.W.;
 RT The transcription termination site at the end of the early region of
 RT bacteriophage T7 DNA.*
 RT J. Virol. 65:2119-2132(1990).
 CC
 CC SEQUENCE OF 1-5 FROM N.A.
 RA MEDLINE=81054683; PubMed=6234001;
 RX Saito H., Tahori S., Temmel F., Richardson C.C.;
 RT Nucleotide sequence of the primary origin of bacteriophage T7 DNA
 RT replication: relationship to adjacent genes and regulatory
 RT elements.*
 RT Proc. Natl. Acad. Sci. U.S.A. 77:3917-3921(1980).
 CC
 CC X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RA MEDLINE=96223302; PubMed=8653795;
 RX Subramanya H.S., Doherty A.J., Ashford S.R., Wigley D.B.;
 RT Crystal structure of an ATP-dependent DNA ligase from bacteriophage
 RT T7.
 RT Cell 86:607-615(1996).
 CC
 CC LYTIC DEVELOPMENT. HAS BEEN IMPLICATED IN T7 DNA REPLICATION AND
 CC GENETIC RECOMBINATION. IT MAY ALSO PLAY A ROLE IN T7 DNA REPAIR.
 CC -1- CATALYTIC ACTIVITY: ATP + (DEOXYRIBONUCLEOTIDE)(N) +
 CC (DEOXYRIBONUCLEOTIDE)(N-M) -> AMP + PYROPHOSPHATE +
 CC -1- STIMULATES RECOMBINATION TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL database
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

Query Match

90.3%; Score 28; DB 1; Length 359;

Best Local Similarity 80.0%; Pred No.1=5+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SWMS 5
 DB 50 SWMS 54
 RESULT 7
 ID YWM_BACSU STANDARD; PRT; 385 AA.
 AC P39596;
 DF 01-FEB-1995 (Rel. 31, Created)
 DT 15-FEB-1995 (Rel. 31, Last sequence update)
 DE HYPOTHEICAL KSL 8 KDA PROTEIN IN EPH-GLK INTERGENIC REGION.
 GN YWM OR 1PB-280.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 CC NCBI_TaxID=1423;
 RA
 RA MEDLINE=95020537; PubMed=7344828;
 RX Glaeser P., Kunst F., Arnard M., Goudart M.P., Gonzales W.,
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
 RA Reseau E., Santana M., Schneider E., Schweizer J., Vertes A.,
 RA Reseau E., Santana M., Schneider E., Schweizer J., Vertes A.,
 RT Bacillus subtilis gene project: cloning and sequencing of the 97
 RT kb region from 325 degrees to 333 degrees.*
 RT Mol. Microbiol. 10:371-384(1993).
 CC
 CC -1- SIMILARITY: TO E.COLI YCDO.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL database
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

EMBL: X73123; CAI51583.1;
 EMBL: 293123; CAI51583.1;
 DR PIR: S39683; S39683;
 DR Subtilist; BG10574; ywm.
 KW Hypothetical protein.
 SQ SEQUENCE 385 AA; 42796 MW; 1P9DC68A385A3C7 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 355;
 Best Local Similarity 80.0%; Pred No.1=7+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SWMS 5
 DB 78 SWMS 82
 RESULT 8
 ID Y306_MYCB STANDARD; PRT; 393 AA.
 AC Y306_MYCB
 DF 01-FEB-1995 (Rel. 33, Created)
 DT 01-FEB-1995 (Rel. 33, Last sequence update)
 DE HYPOTHEICAL PROTEIN MG306.
 GN MG306.
 OS Mycoplasma genitalium.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 CC Mycoplasma; Mycoplasma; Mycoplasma.
 CC NCBI_TaxID=20977;
 RN [1]

SEQUENCE FROM N.A.
 RP STRAIN-ATCC 33530 / G-37;
 RX MEDLINE-6026346; PubMed-7569933;
 RA Frazer C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischman R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fleischman J.L., Weidman J.F., Small K.M., Phillips C.A., Merrick J.H.,
 RA Nguyen P.T., Doughty B.A., Bort K.P., Hu P.-C., Loefer T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT Science 270:397-403(1995).
 RL The minimal gene complement of Mycoplasma genitalium.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC with the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).
 CC EMBL: U97211; AAC71528.1; -.
 DR TIGR: M3306; -.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 15 35 POTENTIAL.
 FT TRANSMEM 56 76 POTENTIAL.
 FT TRANSMEM 86 106 POTENTIAL.
 FT TRANSMEM 134 154 POTENTIAL.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 253 273 POTENTIAL.
 FT TRANSMEM 289 309 POTENTIAL.
 FT TRANSMEM 349 369 POTENTIAL.
 SQ SEQUENCE 393 AA: 45750 MW: D740F8A79EC364A CRC64:
 Query Match 90.3%; Score 28; DB 1; Length 393;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYNVS 5
 DB 173 STWLS 177
 RESULT 9
 YAO6_SCHPO STANDARD; PRT; 455 AA.
 AC Q10085;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHEICAL 49.1 KDA PROTEIN C1D3.06 IN CHROMOSOME I.
 GN SPAC1103.06.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 RN [1] TaxID=4696;
 RP SEQUENCE FROM N.A.
 RC STAIN-972;
 RA Connor R., Church C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases
 RL -1- SUBCELLULAR LOCATION: PROTEIN (POTENTIAL).
 RL -1- STAIN-972 ENTRY.
 CC This STAIN-972 entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).

CC EMBL: 268166; CA92307.1; -.
 DR InterPro: IPR003528; 3.1.
 DR InterPro: IPR003528; 3.1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 44 64 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 FT TRANSMEM 159 179 POTENTIAL.
 FT TRANSMEM 194 204 POTENTIAL.
 FT TRANSMEM 244 264 POTENTIAL.
 FT TRANSMEM 280 300 POTENTIAL.
 FT TRANSMEM 309 329 POTENTIAL.
 FT TRANSMEM 343 363 POTENTIAL.
 FT TRANSMEM 381 401 POTENTIAL.
 FT TRANSMEM 405 425 POTENTIAL.
 SQ SEQUENCE 455 AA: 49086 MW: F741087BC6405327 CRC64:
 Query Match 90.3%; Score 28; DB 1; Length 455;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYNVS 5
 DB 196 STWLS 200
 RESULT 10
 CA34_BOVIN STANDARD; PRT; 471 AA.
 AC Q2808;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE COLLAGEN ALPHA 3(IV) CHAIN (FRAGMENT).
 GN COL4A3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Euteleostomi;
 OC Artiodactyla; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 RN [1] NCBI_TaxID=9913;
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lens;
 RX MEDLINE-91093146; PubMed-1985905;
 RA Morrison E.E., Brown G., Rogers S.T.;
 RT "Morrison E.E., Brown G., Rogers S.T.;
 RT encoding the bovine alpha 3 chain of type IV collagen."
 RL J. Biol. Chem. 266:34-39(1991).
 RN [2]
 RP SEQUENCE OF 227-258.
 RC TISSUE-Kidney;
 RX MEDLINE-91093147; PubMed-2318822;
 RA Noell H., Noell M.E.;
 RT "Glomerular basement membrane. Identification of a fourth chain,
 RT alpha 4, of type IV collagen."
 RL J. Biol. Chem. 265:5466-5469(1990).
 RN [3]
 RP SEQUENCE OF 227-254.
 RX MEDLINE-9830844; PubMed-3417651;
 RA Langerfeld J.P.M., Langerfeld J.P.M., Olinones S., Hudson B.G.;
 RT "Identification of the Goodpasture antigen as the alpha 3(IV) chain
 RT of collagen IV."
 RL J. Biol. Chem. 263:13374-13380(1988).
 RN [4]
 RP SEQUENCE OF 227-244.
 RX MEDLINE-97222419; PubMed-2438983;
 RA Hudson B.G., Langerfeld J.P.M., Wieslander J., Hamilton J.,
 RA Hudson B.G.;
 RT "Localization of the Goodpasture epitope to a novel chain of basement
 RT membrane collagen."
 RL J. Biol. Chem. 267:7874-7877(1997).

OS	Azotriobium caulinodans.
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC	Rhymocitrobium group; Azotriobium.
NCBI_TaxId=7:	
RA	Sequence from N.A.
RP	STRAIN=OHS971:
RC	Mendon K., Michel-Berghelct N., Enormecton S., Kaminski A., Lailja A.,
RA	Cevallos M.A., Elmerich C., Mora J.,
RT	"Poly-beta-hydroxybutyrate turnover in Azotriobium caulinodans is
FT	required for growth and affects nifA expression."
CC	Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
NL	-1- INDUCTION: POLYMERIDES DI-(1-3-HYDROXYBUTYL-COA TO CREATE PHB
CC	END TO END IN THE PRESENCE OF THOUSANDS OF HYDROLYZABLE MOLECULES LINKED
CC	ARMEN CELLS GROW UNDER CONDITIONS OF CELLULAR ENERGY RESERVE MATERIAL
CC	-1- PATHWAY: THIRD STEP IN POLY-BETA-HYDROXYBUTYRATE BIOSYNTHESIS.
CC	-1- SUBCELLULAR LOCATION: CYTOSOL;ER (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE PHA/PHB SYNTHASE FAMILY.
CC	This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Molecular Biology Laboratory. There are no restrictions on its
CC	use by non-profit scientific institutions, provided as a comment is in no way
CC	modified and this statement is not removed or disguised by any means. In all
CC	other cases, permission must be obtained from the copyright owner. For more
CC	or send an email to license@lsdb.slb.ch).
DR	EMBL; AB062377; CAAB0928.1; *
CC	Accession number: AB062377
CC	Accession number: CAAB0928.1
KW	Pbm biosynthesis; Transferrase; 1
KM	Pbm biosynthesis; Transferrase; 1
FT	ACT SITE 320 320 POTENTIAL
SQ	SEQUENCE 583 AA; 64739 MW; C205763D6DDDA18 CRC64;
QY	1 SYMS 54
Db	50 NYMS 54
Query Match	90.3%; Score 28; DB 1; Length 583;
Best Local Similarity	80.0%; Pred. NO. 2.5e+02;
Matches 5	Conservative 1; Mismatches 0; Indels 0; Gaps 0;
RESULT 12	
ID	PRIL_RAT SPANAND; PRI: 745 AA.
PRIL_RAT	063517;
DC	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE
CC	INDUCING RICH PRIMARY RESPONSE)
CC	LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE
CC	Rattus norvegicus (Rat)
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratius.
NCBI_TaxId=10116;	
(1)	
SEQUENCE FROM N.A.	
RP	STRAIN=MISTR; TISSUE=Testis;
RC	SLID=953278603; PUBMED=7758824;
RA	Stromberg J., Bergdman K.E., Post M., Baarends W.M., Thermen A.P.M.,
RT	grouped up a
FT	"Regulation of gene expression in Sertoli cells by
FT	follicle-stimulating hormone (FSH): cloning and characterization of
FT	LRRP, a primary response gene encoding a leucine-rich protein.";
CC	Submitted (Oct-1997) to the EMBL/Genbank/DBJ databases.
NL	-1- INDUCTION: INVOLVED IN THE RESPONSE OF GONADAL TISSUES TO FOLLICLE-
CC	-1- STIMULATING HORMONE.
CC	-1- SUBCELLULAR LOCATION: HIGHLY EXPRESSED IN TESTIS, OVARY AND SPLEEN,
CC	A HIGH CONCENTRATION OF

DR EMBL: M13043; AAA37346.1; -
 DR EMBL: J04448; AAA37437.1; -
 DR EMBL: M13043; GMS48.
 DR MDL: MG158154; GMS48.1.
 DR InterPro: IPR000087; -
 DR Pfam: PF01413; C4; 2.
 DR Pfam: PF01391; Collagen; 21.
 DR KEGG: Extracellular matrix; Connective tissue; Basement membrane;
 KEGG: Signal; Hydroxylation; Glycoprotein; Collagen; Signal.
 FT SIGNAL: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 26

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:12:42 (Search time 81.19 Seconds
(without alignments) 8.148 Million call updates/sec)

Title: US-09-610-118-61

Sequence: 1 SYMS 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archae:.*
2: SP-bacteria:.*
3: SP-fungi:.*
4: SP-human:.*
5: SP-invertebrate:.*
6: SP-mammal:.*
7: SP-mhc:.*
8: SP-organelle:.*
9: SP-phage:.*
10: SP-plant:.*
11: SP-rodent:.*
12: SP-unclassified:.*
13: SP-vertebrate:.*
14: SP-virus:.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	DB ID	Description
1	31	100.0	95	4 Q9ULB6	g9ulb6 Homo sapien
2	31	100.0	942	3 Q13690	Q13690 schizosacch
3	31	100.0	942	10 Q13690	Q13690 schizosacch
4	28	90.3	151	10 Q9KX71	Q9KX71 Arabidopsis
5	28	90.3	151	10 Q9KX71	Q9KX71 Arabidopsis
6	28	90.3	161	11 Q61430	Q61430 mus musculu
7	28	90.3	179	11 P70165	P70165 mus musculu
8	28	90.3	185	5 Q45206	Q45206 schistosoma
9	28	90.3	191	5 Q45206	Q45206 schistosoma
10	28	90.3	191	5 Q45206	Q45206 schistosoma
11	28	90.3	191	5 Q45206	Q45206 schistosoma
12	28	90.3	191	5 Q45206	Q45206 schistosoma
13	28	90.3	202	6 Q28272	Q28272 canis fami
14	28	90.3	203	6 Q28682	Q28682 oryctolagus
15	28	90.3	203	6 Q29032	Q29032 sus scrofa
16	28	90.3	204	2 Q9KRD0	Q9KRD0 vltro chol
17	28	90.3	205	6 Q28274	Q28274 canis fami
18	28	90.3	206	8 Q21463	Q21463 mytilus t
19	28	90.3	206	8 Q21463	Q21463 mytilus t

20	28	90.3	206	8 Q21464	Q21464 mytilus t
21	28	90.3	207	8 Q28273	Q28273 canis fami
22	28	90.3	212	6 Q28512	Q28512 macaca m
23	28	90.3	212	6 Q28567	Q28567 ovis arie
24	28	90.3	216	2 Q9X0M5	Q9X0M5 thermotoga
25	28	90.3	225	6 Q28271	Q28271 canis fami
26	28	90.3	226	4 Q9KX71	Q9KX71 Arabidopsis
27	28	90.3	229	4 Q9KX71	Q9KX71 Arabidopsis
28	28	90.3	230	10 Q9KX71	Q9KX71 Arabidopsis
29	28	90.3	230	10 Q9KX71	Q9KX71 Arabidopsis
30	28	90.3	245	4 Q9KX71	Q9KX71 Arabidopsis
31	28	90.3	245	4 Q9KX71	Q9KX71 Arabidopsis
32	28	90.3	246	11 Q61435	Q61435 mus musculu
33	28	90.3	253	11 Q61435	Q61435 mus musculu
34	28	90.3	254	2 Q91652	Q91652 pseudomonas
35	28	90.3	256	2 Q9KX71	Q9KX71 Arabidopsis
36	28	90.3	272	11 Q9KX71	Q9KX71 Arabidopsis
37	28	90.3	312	4 Q9KX71	Q9KX71 Arabidopsis
38	28	90.3	338	4 Q9KX71	Q9KX71 Arabidopsis
39	28	90.3	349	2 Q9KX71	Q9KX71 Arabidopsis
40	28	90.3	349	2 Q9KX71	Q9KX71 Arabidopsis
41	28	90.3	382	5 Q9KX71	Q9KX71 Arabidopsis
42	28	90.3	394	2 Q9KX71	Q9KX71 Arabidopsis
43	28	90.3	398	10 Q9KX71	Q9KX71 Arabidopsis
44	28	90.3	398	10 Q9KX71	Q9KX71 Arabidopsis
45	28	90.3	426	2 Q9KX71	Q9KX71 Arabidopsis

ALIGNMENTS

RESULT 1
Q9ULB6 PRELIMINARY: PRT: 95 AA.

AC Q9ULB6
DT 01-MAY-2000 (TRFMBLrel. 13, Created)
DT 01-MAY-2000 (TRFMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRFMBLrel. 16, Annotation update)
DE IMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.:
RT Human VA gene sequence.
RT Human VA gene sequence.
CC - SIMILARITY: NO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC - DOMAIN.
DR EMBL: AB032688; BAA87067.1; -
DR HSSP: P01772; 2F84.
DR InterPro: IPR003966; -
DR InterPro: IPR003966; -
DR IAS: IPR003966; -
DR SMART: SM00406; 1; 1.
FT NON_TER 95
FT NON_TER 95
SQ SEQUENCE 95 AA: 10527 MW: 90A8C6D16D22574A CCKC4;

Query Match 100.0%; Score 31; DB 4; Length 95;
Database Match 100.0%; Pred No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 30 SYMS 34
RESULT 2
013690

Query Match 90.3%; Score 28; DB 10; Length 151;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 SYNMS 5
 11111
 Db 130 SYNMT 134

RESULT 6

ID 061430 PRELIMINARY: PRT: 161 AA.
 AC 061430-
 DT 01-NOV-1996 (TREMBLER). 01, Created)
 DT 01-NOV-1996 (TREMBLER). 01, Last sequence update)
 DE 01-MAR-2001 (TREMBLER). 16, Last annotation update)
 DE COLLAGEN TYPE IV ALPHA3 CHAIN (FRAGMENT).
 GN COL4A3.
 OS Mus musculus (Mouse)
 OC Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerognathii; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX 11
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Overhauled; T.: 1994 to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 DR InterPro: IPR000504; -;
 DR InterPro: IPR001442; -;
 DR Pfam: PF01413; C4; 2;
 DR PROSITE: PS00303; RNP-1; UNKNOWN_1.
 DR SMART: SM00111; C4; 1;
 FT NON-TER 1 161
 FT CDS 1 161
 SEQUENCE 161 AA: 117925 MW: 1f59D6CFEB236CS CRC64;

Query Match 90.3%; Score 28; DB 11; Length 161;
 Best Local Similarity 80.0%; Pred. No. 3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 SYNMS 5
 11111
 Db 29 SYNMS 33

RESULT 7

ID P70165 PRELIMINARY: PRT: 179 AA.
 AC P70165-
 DT 01-FEB-1997 (TREMBLER). 02, Created)
 DT 01-FEB-1997 (TREMBLER). 02, Last sequence update)
 DE 01-MAR-2001 (TREMBLER). 16, Last annotation update)
 DE COLLAGEN TYPE IV ALPHA5 CHAIN (FRAGMENT).
 GN COL4A5.
 OS Mus musculus (Mouse)
 OC Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerognathii; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX 11
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Overhauled (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X8218; CAA57698.1;
 DR InterPro: IPR001442; -;
 DR Pfam: PF01413; C4; 2;
 DR SMART: SM00111; C4; 1;
 FT NON-TER 1 179
 FT CDS 1 179
 SEQUENCE 179 AA: 19859 MW: 20A188F5687582F CRC64;

Query Match 90.3%; Score 28; DB 11; Length 179;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 SYNMS 5
 11111
 Db 57 SYNMS 61

RESULT 8

ID 045206 PRELIMINARY: PRT: 185 AA.
 AC 045206-
 DT 01-JUN-1998 (TREMBLER). 06, Created)
 DT 01-JUN-1998 (TREMBLER). 06, Last sequence update)
 DE 01-MAR-2001 (TREMBLER). 16, Last annotation update)
 DE 5221.7b ANTIEN.
 GN 5221.7b ANTIEN.
 OS Schistosoma (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigoidae; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 NCBI_TaxID=6182;
 RX 11
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHILIPPINE (MINDORO);
 RA Hefalla J.C., Alamaras J.A., Acosta L.P., Ramirez B.L., Santiago M.L.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO EP-HAND FAMILY.
 DR EMBL: AF048759; AAC13358.1; -;
 DR InterPro: IPR000280; -;
 DR PROSITE: PS00018; EF-HAND; UNKNOWN_1.
 DR SMART: SM00054; EF-HAND; UNKNOWN_1.
 SEQUENCE 185 AA: 21693 MW: 67B8CDD2E2B84855 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 185;
 Best Local Similarity 80.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 SYNMS 5
 11111
 Db 155 SYNMS 159

RESULT 9

ID 044372 PRELIMINARY: PRT: 191 AA.
 AC 044372-
 DT 01-JUN-1998 (TREMBLER). 06, Created)
 DT 01-JUN-1998 (TREMBLER). 06, Last sequence update)
 DE 01-MAR-2001 (TREMBLER). 16, Last annotation update)
 DE Schistosoma japonicum (Blood fluke).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigoidae; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 NCBI_TaxID=6182;
 RX 11
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=MINDORO;
 RA Santiago M.L., Hefalla J.C.R., Kurtis J.D., Wiest P.M., Olds G.R.,
 DL Dunne D.W., Ramirez B.L.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO EP-HAND FAMILY.
 DR EMBL: AF030484; AAC67308.1; -;
 DR InterPro: IPR000361; efhand; 2;
 DR PROSITE: PS00018; EF-HAND; UNKNOWN_1.
 DR SMART: SM00054; EF-HAND; UNKNOWN_1.
 SEQUENCE 191 AA: 20A188F5687582F CRC64;

Db 161 SYMMS 165

RESULT 13

AC Q28272 PRELIMINARY: PRT: 202 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE COLLAGEN TYPE IV ALPHA 2 CHAIN (FRAGMENT).

GN COL4A3

DR InterPro: IP8001442; -

DR EMBL: U05934; AA04584.1; -

DR SMART: SM00111; C4; 1.

FT NON_TER 1 202

PT SEQUENCE 202 AA: 22079 MW: 25A56E7642A329FC CRC64:

SQ

Query Match

Best Local Similarity 80.0%; Score 28; DB 6; Length 203;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMMS 5

Db 70 SYMMS 74

RESULT 14

AC Q28682 PRELIMINARY: PRT: 203 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE COLLAGEN TYPE IV COLLAGEN (FRAGMENT).

GN COL4A3

DR InterPro: IP8001442; -

DR EMBL: U05934; AA04584.1; -

DR SMART: SM00111; C4; 1.

FT NON_TER 1 203

PT SEQUENCE 203 AA: 22213 MW: E14173816E4D9E30 CRC64:

SQ

Query Match

Best Local Similarity 80.0%; Score 28; DB 6; Length 203;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMMS 5

Db 62 SYMMS 66

Query Match 90.3%; Score 28; DB 6; Length 203;
 Best Local Similarity 80.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMMS 5

Db 62 SYMMS 66

RESULT 15

AC Q29032 PRELIMINARY: PRT: 203 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE ALPHA-3 TYPE IV COLLAGEN (FRAGMENT).

GN COL4A3

DR InterPro: IP8001442; -

DR EMBL: U05934; AA04584.1; -

DR SMART: SM00111; C4; 1.

FT NON_TER 1 203

PT SEQUENCE 203 AA: 22326 MW: E3B20E32D9A245A5A CRC64:

SQ

Query Match

Best Local Similarity 80.0%; Score 28; DB 6; Length 203;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMMS 5

Db 62 SYMMS 66

Search completed: November 19, 2001, 08:25:00

Job time: 738 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:11:07 ; Search time 77.92 Seconds
(without alignments)
3.890 Million cell updates/sec

Title: US-09-610-118-61

Sequence: 1 SYWMS 5

Sequence: 1 SYWMS 5

Scoring code: 00000000
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

```
Minimum DB seq length: 0
```

Maximum DB seq length: 2000000000

Post-processing:	Minimum Match	0%
Maximum Match	100%	

Listing first 45 summaries

Database : A_Geneseq_0601:1
1 : /STNCR/arcdata

- 1: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1180./ DAT *
- 2: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1181./ DAT *
- 3: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1182./ DAT *
- 4: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1183./ DAT *
- 5: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1184./ DAT *
- 6: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1185./ DAT *
- 7: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1186./ DAT *
- 8: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1187./ DAT *
- 9: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1188./ DAT *
- 10: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1189./ DAT *
- 11: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1190./ DAT *
- 12: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1191./ DAT *
- 13: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1192./ DAT *
- 14: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1193./ DAT *
- 15: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1194./ DAT *
- 16: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1195./ DAT *
- 17: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1196./ DAT *
- 18: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1197./ DAT *
- 19: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1198./ DAT *
- 20: /S1D58./g5gdgdat1./geneseq./geneseqP./AA1199./ DAT *
- 21: /S1D58./g5gdgdat1./geneseq./geneseqP./AA2000./ DAT *
- 22: /S1D58./g5gdgdat1./geneseq./geneseqP./AA2001./ DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

[illegible]

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																																																																																																																																																																	
AA8594316	AA8594317	AA8594318	AA8594319	AA8594320	AA8594321	AA8594322	AA8594323	AA8594324	AA8594325	AA8594326	AA8594327	AA8594328	AA8594329	AA8594330	AA8594331	AA8594332	AA8594333	AA8594334	AA8594335	AA8594336	AA8594337	AA8594338	AA8594339	AA8594340	AA8594341	AA8594342	AA8594343	AA8594344	AA8594345	AA8594346	AA8594347	AA8594348	AA8594349	AA8594350	AA8594351	AA8594352	AA8594353	AA8594354	AA8594355	AA8594356	AA8594357	AA8594358	AA8594359	AA8594360	AA8594361	AA8594362	AA8594363	AA8594364	AA8594365	AA8594366	AA8594367	AA8594368	AA8594369	AA8594370	AA8594371	AA8594372	AA8594373	AA8594374	AA8594375	AA8594376	AA8594377	AA8594378	AA8594379	AA8594380	AA8594381	AA8594382	AA8594383	AA8594384	AA8594385	AA8594386	AA8594387	AA8594388	AA8594389	AA8594390	AA8594391	AA8594392	AA8594393	AA8594394	AA8594395	AA8594396	AA8594397	AA8594398	AA8594399	AA8594400	AA8594401	AA8594402	AA8594403	AA8594404	AA8594405	AA8594406	AA8594407	AA8594408	AA8594409	AA8594410	AA8594411	AA8594412	AA8594413	AA8594414	AA8594415	AA8594416	AA8594417	AA8594418	AA8594419	AA8594420	AA8594421	AA8594422	AA8594423	AA8594424	AA8594425	AA8594426	AA8594427	AA8594428	AA8594429	AA8594430	AA8594431	AA8594432	AA8594433	AA8594434	AA8594435	AA8594436	AA8594437	AA8594438	AA8594439	AA8594440	AA8594441	AA8594442	AA8594443	AA8594444	AA8594445	AA8594446	AA8594447	AA8594448	AA8594449	AA8594450	AA8594451	AA8594452	AA8594453	AA8594454	AA8594455	AA8594456	AA8594457	AA8594458	AA8594459	AA8594460	AA8594461	AA8594462	AA8594463	AA8594464	AA8594465	AA8594466	AA8594467	AA8594468	AA8594469	AA8594470	AA8594471	AA8594472	AA8594473	AA8594474	AA8594475	AA8594476	AA8594477	AA8594478	AA8594479	AA8594480	AA8594481	AA8594482	AA8594483	AA8594484	AA8594485	AA8594486	AA8594487	AA8594488	AA8594489	AA8594490	AA8594491	AA8594492	AA8594493	AA8594494	AA8594495	AA8594496	AA8594497	AA8594498	AA8594499	AA8594500	AA8594501	AA8594502	AA8594503	AA8594504	AA8594505	AA8594506	AA8594507	AA8594508	AA8594509	AA8594510	AA8594511	AA8594512	AA8594513	AA8594514	AA8594515	AA8594516	AA8594517	AA8594518	AA8594519	AA8594520	AA8594521	AA8594522	AA8594523	AA8594524	AA8594525	AA8594526	AA8594527	AA8594528	AA8594529	AA8594530	AA8594531	AA8594532	AA8594533	AA8594534	AA8594535	AA8594536	AA8594537	AA8594538	AA8594539	AA8594540	AA8594541	AA8594542	AA8594543	AA8594544	AA8594545	AA8594546	AA8594547	AA8594548	AA8594549	AA8594550	AA8594551	AA8594552	AA8594553	AA8594554	AA8594555	AA8594556	AA8594557	AA8594558	AA8594559	AA8594560	AA8594561	AA8594562	AA8594563	AA8594564	AA8594565	AA8594566	AA8594567	AA8594568	AA8594569	AA8594570	AA8594571	AA8594572	AA8594573	AA8594574	AA8594575	AA8594576</

ALIGNMENTS

RESULT 1

ID AAB61293 standard; Peptide; 5 AA

AC AAB61293;

DT 04-APR-2001 (first entry)

DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 61

KW Human; antibody; scFv; CDR; complementarity determining region;

KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein V

KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke; liver disease; immunological disease; liver disorder

KN cancer.

OS Homo sapiens

PN WO200100810-A1

PD 04-JAN-2001.
XX

PF 30-JUN-2000; 2000WO-US18152.
YY

PR	30-JUN-1999;	99US-0345468
PR	06-DEC-1999;	99US-0454824

PR 14-FEB-2000; 200005-050338 /
YYPA (MILL-) MILLENNIUM PHARM INC
YY

PI . Bustleld SJ, Villeral J, Jandroel-Pellus M, Valmicheva M, Villal

PI Qian MD, Kingsbury G

PI Melachian SM, Rapoport B.
 XX
 XX NPL: 1995-13383/18.
 DR N-PSDB: AA089332.
 XX
 XX Graves' ophthalmopathy-associated monoclonal antibody - produced
 PT by monoclonal cloning of immunoglobulin genes by PCR
 XX
 XX Disclosure: Page 72: 94pp: English.
 PS
 XX L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC fragments and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained. 2/12 clones of H chain and 1/12 clones of L chain
 CC were sequenced. The H chain sequence (AA089332) which encodes
 CC the protein given in AA872074. The DNA (AA089333) and corresp. amino
 CC acid (AA872075) sequences of the VH region of a representative clone,
 CC OFH1.19, are provided.
 XX
 XX Sequence 98 AA:
 SO
 Query Match 100.0%; Score 31; DB 16; Length 98;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SYNMS 5
 DB 31 SYNMS 35
 XX
 XX RESULT 4
 XX ID AAB40138 standard; Protein: 98 AA.
 XX AAB40138:
 XX
 XX 05-FEB-2001 (first entry)
 XX
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 664.
 DE
 XX Human: neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 XX complementarily determining region; CDR; antirheumatic; antiallergic;
 XX antileukemic; neuroprotective; antiparasitic; antiparasitic; candidant;
 XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 XX multiple sclerosis; rheumatoid arthritis.
 XX
 XX Homo sapiens.
 XX WO2000056772-A1.
 XX
 XX 28-SEP-2000.
 XX
 XX 24-MAR-2000: 2000MO-US07946.
 XX
 XX 25-MAR-1999: 99US-0126603.
 XX
 XX (BADI) BASF AG.
 XX (GENM) GENETICS INST INC.
 XX
 XX Salfield JG, Boguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakçalan Z, Labkovsky B, Sakoratzas P, Friedlich S, Myles A;
 PI Veidman GM, Venturini A, Warne NW, Widom A, Elyin JG, Duncan AR;
 PI Derbyshtre EJ, Carmen S, Smith S, Hollet TL, Du Fou SL.
 XX WPI: 2000-638250/61.
 XX
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX
 XX Claim 75: Page 122: 377pp: English.
 XX
 XX This invention relates to a new human antibody specific for human

CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AA839485-839516 representing
 CC anti-IL-12 antibody heavy and light chain variable regions determining
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AA839517-839560 and AAB40068-B40149. Sequences AA839561-839771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AA839772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are a neutralizing
 CC AAB40062 CDR3 primer and a non-neutralizing AAB40063 primer.
 CC Antiinflammatory; neuroprotective; antiparasitic; antileukemic;
 CC antirheumatic; antiallergic; antiparasitic; antiparasitic; antiparasitic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12, arthritis,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 XX
 XX Sequence 98 AA:
 SO
 Query Match 100.0%; Score 31; DB 21; Length 98;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SYNMS 5
 DB 31 SYNMS 35
 XX
 XX RESULT 5
 XX ID AAB40140 standard; Protein: 98 AA.
 XX AAB40140:
 XX
 XX 05-FEB-2001 (first entry)
 XX
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 666.
 DE
 XX Human: neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 XX complementarily determining region; CDR; antirheumatic; antiallergic;
 XX antileukemic; neuroprotective; antiparasitic; antiparasitic; candidant;
 XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 XX multiple sclerosis; rheumatoid arthritis.
 XX
 XX Homo sapiens.
 XX WO2000056772-A1.
 XX
 XX 28-SEP-2000.
 XX
 XX 24-MAR-2000: 2000MO-US07946.
 XX
 XX 25-MAR-1999: 99US-0126603.
 XX
 XX (BADI) BASF AG.
 XX (GENM) GENETICS INST INC.
 XX
 XX Salfield JG, Boguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakçalan Z, Labkovsky B, Sakoratzas P, Friedlich S, Myles A;
 PI Veidman GM, Venturini A, Warne NW, Widom A, Elyin JG, Duncan AR;
 PI Derbyshtre EJ, Carmen S, Smith S, Hollet TL, Du Fou SL.
 XX WPI: 2000-638250/61.
 XX
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX
 XX Claim 75: Page 122: 377pp: English.
 XX
 XX This invention relates to a new human antibody specific for human

Db 32 syms 36

|||||

RESULT 8

AA062778 standard; Protein: 123 AA.

AA062778:

03-APR-2001 (first entry)

Human HIV-1 monoclonal antibody SEQ ID NO: 77.

Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

envelope glycoprotein; gp120; diagnosis.

Homo sapiens.

W0200100678-A1.

04-JAN-2001.

23-JUN-2000: 2000MO-US17327.

30-JUN-1999: 9905-0141701.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Watkins BA, Reitz MS;

WPI: 2001-112438/12.

N-PSDB: AAF29079.

Novel human monoclonal antibody immunoreactive with human

immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

in biological sample and providing passive immunotherapy to HIV-1

infected mammal.

Claim 1: Page 71; 81pp; English.

The present invention provides the protein and coding sequences for the

variable regions of human monoclonal antibodies which are immunoreactive

with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

These can be used in diagnosis and therapy of HIV-1 infection.

Sequence 123 AA:

Query Match 100.0%; Score 31; DB 22; Length 123;

Best Local Similarity 100.0%; Pred. No. 64;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5

DB 32 syms 36

RESULT 9

AA062776 standard; Protein: 125 AA.

AA062776:

03-APR-2001 (first entry)

Human HIV-1 monoclonal antibody SEQ ID NO: 75.

Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

envelope glycoprotein; gp120; diagnosis.

Homo sapiens.

W0200100678-A1.

04-JAN-2001.

23-JUN-2000: 2000MO-US17327.

30-JUN-1999: 9905-0141701.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Watkins BA, Reitz MS;

WPI: 2001-112438/12.

N-PSDB: AAF29077.

Novel human monoclonal antibody immunoreactive with human

immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

in biological sample and providing passive immunotherapy to HIV-1

infected mammal.

Claim 1: Page 69-70; 81pp; English.

The present invention provides the protein and coding sequences for the

variable regions of human monoclonal antibodies which are immunoreactive

with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

These can be used in diagnosis and therapy of HIV-1 infection.

Sequence 125 AA:

Query Match 100.0%; Score 31; DB 22; Length 125;

Best Local Similarity 100.0%; Pred. No. 64;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5

DB 32 syms 36

RESULT 10

AA090180 standard; Protein: 271 AA.

AA090180:

10-MAY-1999 (first entry)

Human clone A6 fusion protein antibody.

Antibody: human; clone A6; has: fusion protein; polyclonal tag;

Western blot; enzyme-linked immunosorbent assay; ELISA; therapy;

immunofluorescence; immunoprecipitation assay; affinity purification;

diagnosis; vaccine; serum; immune response.

Homo sapiens.

W09901475-A2.

14-JAN-1999.

03-JUL-1998: 98WO-DE01882.

04-JUL-1997: 97DE-1028697.

(DEKAT-) DEUT KRESFORSCHUNGSZENTRUM.

Braunagel M, Doersam H, Kiprijanov S, Kuetschner T;

Little M, Welschhof M;

CC are derived from mouse monoclonal antibody FWP51 (BCAC 90112118)
 CC directed to the human growth factor receptor HER2. The scv is
 CC used as the tumour antigen binding domain of a bifunctional protein
 CC that is expressed in cytotoxic T-lymphocytes (CTLs), allowing
 CC adoptive immunotherapy of cancer.

SO Sequence 5 AA:

Query Match 90.3%; Score 28; DB 16; Length 5;
 Best Local Similarity 80.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYNVS 5
 :|||||
 DB 1 SYNVS 5

RESULT 13

AA897316 standard; peptide; 5 AA.

AA897316:

15-OCT-1996 (first entry)

Humanised monoclonal antibody heavy chain CDR.

Monoclonal antibody: humanised; mouse; framework region: FR; CDR:

complementary determining region: anti-carcinoembryonic antigen;

CEA; diagnosis: imaging; therapy: immune response.

Mus musculus.

W03611013-A1.

18-APR-1996.

28-SEP-1995; 95WO-US11964.

05-OCT-1994; 94US-0318157.

(IMMUN-) IMMUNOMEDICS INC.

Armour KL, Hansen RJ;

WPI: 1996-209653/21.

New humanised anti-CEA monoclonal antibody - having engrafted murine
 CDRs, used for diagnosis, imaging and therapy of CEA-producing
 cancers

Claim 5: Page 38; 62pp; English.

New humanised monoclonal antibodies (MAbs) comprising the
 complementary determining regions (CDRs) of a parental murine class
 II anti-carcinoembryonic (CEA) antibody which can be derived from
 CC an anti-CEA monoclonal antibody, and a human CDR region of the
 CC of the parental murine MAbs but are less immunogenic in a human
 CC subject than the parental MAbs. The humanised antibodies can be used
 CC in diagnosis, imaging and therapy of CEA-producing cancers and
 CC patients receiving the humanised antibodies and conjugates show
 CC improved therapeutic results compared to patients receiving the
 CC parental antibodies. The humanised antibodies are compared to the parent
 CC antibody. This sequence is a murine derived CDR region which
 CC corresponds to CDR 1 in the heavy chain of the humanised MAbs. See
 CC AA897313-97333.

Sequence 5 AA:

Query Match 90.3%; Score 28; DB 17; Length 5;

Best Local Similarity 80.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYNVS 5
 :|||||
 DB 1 SYNVS 5

RESULT 14

AA105038 standard; peptide; 5 AA.

AA105038:

16-JUN-1999 (first entry)

Tumour antigen antibody heavy chain CDR1 clone F15.

Tumour antigen: antibody; CDR: complementarity determining region;

binding molecule identification: tumour-specific binding polypeptide;

cancer therapy: heavy chain.

Homo sapiens.

W03906834-A2.

11-FEB-1999.

04-AUG-1998; 98MO-US16280.

04-AUG-1997; 97US-0905825.

04-AUG-1997; 97US-1112222.

(IXSY-) IXSYS INC.

Huse WD, Watkins JD, Wu H;

WPI: 1999-153951/13.

N-PSDB: AAX28215.

Identifying binding molecules for ligands, particularly tumour
 PT antigens, by selectively immobilising a population of binding
 PT molecules to a solid support and screening for binding to two or
 PT more ligands

Claim 15: Page 60; 80pp; English.

This sequence represents a heavy chain complementarity determining
 CC region (CDR) from a tumour antigen specific antibody.
 CC The invention relates to a method for identifying a binding molecule
 CC having selective affinity for a ligand comprising: (a) selectively
 CC immobilising a diverse population of binding molecules to a solid
 CC support; (b) simultaneously contacting the diverse population immobilised
 CC on the solid support with 2 or more ligands; and (c) selecting the
 CC one binding molecule that allows for the rapid and efficient methods for
 CC identification of binding molecules which exhibit selective affinity for
 CC one or more ligands of interest. They are used particularly for
 CC identifying tumour-specific binding polypeptides which can be used as
 CC targeting agents for cancer therapy that minimises impact on non-tumour
 CC tissues.

Sequence 5 AA:

Query Match 90.3%; Score 28; DB 20; Length 5;
 Best Local Similarity 80.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYNVS 5
 :|||||
 DB 1 SYNVS 5

Search completed: November 19, 2001, 08:12:34
 Job time: 87 sec

```

RESULT 15
AAV64781
ID AAV64781 standard: Protein: 59 AA.
XX
AC AAV64781;
XX
DT 01-FEB-2000 (first entry)
XX
DE Human 5' EST related polypeptide SEQ ID NO:942.
XX
KW Human: 5' EST: expressed sequence tag; secreted protein; diagnosis;
KW gene therapy; chromosome mapping; upstream regulatory sequence;
KW forensic; location; development; protein synthesis; stability;
KW regulation; identification.
XX
OS Homo sapiens.
XX
PN M09953051-A2.
XX
PD 21-OCT-1999.
XX
PR 09-APR-1999; 99MO-1B00712.
XX
PR 09-APR-1998; 98US-0057719.
XX
PR 28-APR-1998; 98US-0069047.
XX
XX (GEST ) GENSET.
XX
XX Dumas Mline Edwards J, Duclert A, Giordano J;
XX
XX WPI: 2000-038446/03.
XX
XX N-PSDB; AA242395.
XX
XX Novel secreted protein 5' expressed sequence tag sequences used in
XX diagnostic, forensic, gene therapy, and chromosome mapping procedures
XX
XX Claim 3; Page 641; 837pp; English.
XX
XX AA24265 to AA243075 represent novel 5' expressed sequence tag (EST)
XX sequences, corresponding to human secreted proteins. AAV6451 to
XX AAV6458 represent the EST-related proteins corresponding to AA24265 to
XX AA24302. The 5' ESTs can be used for producing secreted human gene
XX products. They can be used to identify and isolate 5' untranslated
XX regions and upstream regulatory regions which control the
XX location, development, expression, and stability of mRNA. The ESTs are
XX well as stability of mRNA. The ESTs are also used to identify
XX chromosome mapping, and to obtain full length cDNA clones. The ESTs can
XX also be used in forensic procedures to identify individuals, or in
XX resulting from abnormal gene expression. The products may also be used in
XX diagnostic procedures to identify individuals having genetic diseases
XX CC used for diagnostic purposes. The nucleic acids encoding a polypeptide can be
XX CC insertion of a polypeptide into a secreted protein, or in
XX CC into a cell. The proteins encoded by the EST sequences may be useful in
XX CC treating a variety of human conditions. Secreted proteins have
XX CC variable, AA24229 to AA24264 and AAV6464 to AAV64650 represent
XX CC sequences used in the exemplification of the present invention.
XX
XX Sequence 59 AA:
XX
Query Match 90.3%; Score 28; DB 21; Length 59;
Went Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYNMS 5
||||:
Db 50 symtc 54

```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: November 19, 2001, 08:11:07 : Search time 526.89 Seconds
(without alignments)
2.635 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 STWMS 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA>Main.*
1: /cgn2.6/prodata/2/paa/US06.COMB.pep.*
2: /cgn2.6/prodata/2/paa/US06.COMB.pep.*
3: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
4: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
5: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
6: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
7: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
8: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
9: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
10: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
11: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
12: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
13: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
14: /cgn2.6/prodata/2/paa/US08.COMB.pep.*
15: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
16: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
17: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
18: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
19: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
20: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
21: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
22: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
23: /cgn2.6/prodata/2/paa/US09.COMB.pep.*
24: /cgn2.6/prodata/2/paa/US09.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best results printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	5	1	Sequence 61, Appl
2	31	100.0	5	20	Sequence 61, Appl
3	31	100.0	5	22	Sequence 61, Appl
4	31	100.0	27	24	Sequence 3529, Appl
5	31	100.0	73	24	Sequence 4861, Ap
6	31	100.0	58	1	Sequence 664, App
7	31	100.0	98	1	Sequence 664, App
8	31	100.0	98	1	Sequence 32, Appl
9	31	100.0	98	8	Sequence 32, Appl

10	31	100.0	98	8	US-08-486-202-32
11	31	100.0	98	19	US-09-534-717-664
12	31	100.0	98	19	US-09-534-717-664
13	31	100.0	98	21	US-09-756-455-598
14	31	100.0	123	24	US-60-141-701-76
15	31	100.0	123	24	US-60-141-701-76
16	31	100.0	123	24	US-60-141-701-76
17	31	100.0	123	24	US-60-141-701-76
18	31	100.0	123	24	US-60-141-701-76
19	31	100.0	123	24	US-60-141-701-76
20	31	100.0	123	24	US-60-141-701-76
21	31	100.0	123	24	US-60-141-701-76
22	31	100.0	123	24	US-60-141-701-76
23	31	100.0	123	24	US-60-141-701-76
24	31	100.0	123	24	US-60-141-701-76
25	31	100.0	123	24	US-60-141-701-76
26	31	100.0	123	24	US-60-141-701-76
27	31	100.0	123	24	US-60-141-701-76
28	31	100.0	123	24	US-60-141-701-76
29	31	100.0	123	24	US-60-141-701-76
30	31	100.0	123	24	US-60-141-701-76
31	31	100.0	123	24	US-60-141-701-76
32	31	100.0	123	24	US-60-141-701-76
33	31	100.0	123	24	US-60-141-701-76
34	31	100.0	123	24	US-60-141-701-76
35	31	100.0	123	24	US-60-141-701-76
36	31	100.0	123	24	US-60-141-701-76
37	31	100.0	123	24	US-60-141-701-76
38	31	100.0	123	24	US-60-141-701-76
39	31	100.0	123	24	US-60-141-701-76
40	31	100.0	123	24	US-60-141-701-76
41	31	100.0	123	24	US-60-141-701-76
42	31	100.0	123	24	US-60-141-701-76
43	31	100.0	123	24	US-60-141-701-76
44	31	100.0	123	24	US-60-141-701-76
45	31	100.0	123	24	US-60-141-701-76

ALIGNMENTS

RESULT 1
PCT-US000-18152-61
Sequence 61, Application PCT/US00018152
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
CURRENT FILING DATE: 2000-06-30
CURRENT FILING DATE: 2000-06-30
CURRENT FILING DATE: 2000-06-30
EARLIER FILING DATE: 09/503,387
EARLIER FILING DATE: 12/6/99/09/745,468
EARLIER FILING DATE: 6/30/99
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 61
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US000-18152-61

Query Match 100.0%; Score 31; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e06;
Matches 5; Conservative 0; Mismatches 0; Indeals 0; Gaps 0;

DB 1 STWMS 5

Sequence 32, Appl
Sequence 664, App
Sequence 664, App
Sequence 88, Appl
Sequence 598, Appl
Sequence 76, Appl
Sequence 77, Appl
Sequence 79, Appl
Sequence 10, Appl
Sequence 73, Appl
Sequence 1822, A
Sequence 1822, A
Sequence 1889, Ap
Sequence 1889, Ap
Sequence 1470, Ap
Sequence 1534, Ap
Sequence 10, App
Sequence 10, App
Sequence 4698, App
Sequence 3861, A
Sequence 48095, A
Sequence 21288, A
Sequence 472, App
Sequence 23112, App
Sequence 18292, A
Sequence 18292, A
Sequence 30906, A

RESULT 2
US-09-610-118-61

```

: Sequence 61, Application US/09610118
: GENERAL INFORMATION:
: APPLICANT: Buefield, S.
: APPLICANT: Villevial, J.
: APPLICANT: Jandrot-Perrus, M.
: APPLICANT: Valchenker, W.
: APPLICANT: Gilm, M.
: APPLICANT: K. Gilm, M.
: TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
: FILE REFERENCE: 7861-211
: CURRENT APPLICATION NUMBER: US/09/610.118
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 09/503.387
: PRIOR FILING DATE: 2/14/00
: PRIOR APPLICATION NUMBER: 09/454.824
: PRIOR FILING DATE: 12/29/99
: PRIOR APPLICATION NUMBER: 09/345.468
: PRIOR FILING DATE: 6/30/99
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO: 61
: LENGTH: 51
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-610-118-61

```

Query Match
Best Local Similarity: 100.0%; Score 31; DB 20; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 1 SYMS 5

```

RESULT 3
US-09-832-312-61
: Sequence 61, Application US/09832312
: GENERAL INFORMATION:
: APPLICANT: Buefield et al.
: TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
: FILE REFERENCE: 7861-211
: CURRENT APPLICATION NUMBER: US/09/832.312
: PRIOR FILING DATE: 2001-04-09
: PRIOR APPLICATION NUMBER: 09/610.118
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 09/503.387
: PRIOR FILING DATE: 2000-02-14
: PRIOR APPLICATION NUMBER: 09/454.824
: PRIOR FILING DATE: 12/29/99
: PRIOR APPLICATION NUMBER: 09/345.468
: PRIOR FILING DATE: 1999-06-30
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO: 61
: LENGTH: 51
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-832-312-61

```

Query Match
Best Local Similarity: 100.0%; Score 31; DB 22; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 1 SYMS 5

RESULT 4
US-60-160-209-3528

```

: Sequence 3528, Application US/60160209
: GENERAL INFORMATION:
: APPLICANT: BONAZZI, VIVIAN
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
: FILE REFERENCE: C1000113
: CURRENT APPLICATION NUMBER: US/60/160.209
: CURRENT FILING DATE: 1999-10-19
: NUMBER OF SEQ ID NOS: 4646
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 3528
: LENGTH: 27
: TYPE: PRT
: ORGANISM: HUMAN
US-60-160-209-3528

```

Query Match
Best Local Similarity: 100.0%; Score 31; DB 24; Length 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 17 SYMS 21

```

RESULT 5
US-60-160-203-4861
: Sequence 4861, Application US/60160203
: GENERAL INFORMATION:
: APPLICANT: BONAZZI, VIVIAN
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
: USES THEREOF
: FILE REFERENCE: C1000116
: CURRENT APPLICATION NUMBER: US/60/160.203
: CURRENT FILING DATE: 1999-10-19
: NUMBER OF SEQ ID NOS: 6374
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 4861
: LENGTH: 73
: TYPE: PRT
: ORGANISM: HUMAN
US-60-160-203-4861

```

Query Match
Best Local Similarity: 100.0%; Score 31; DB 24; Length 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 53 SYMS 57

```

RESULT 6
PCT-US00-07946-664
: Sequence 664, Application PC/TUS007946
: GENERAL INFORMATION:
: APPLICANT: JOHNSON, SAIFELD et al.
: TITLE OF INVENTION: ANTIBODIES THAT BIND HUMAN IL-12 AND METHODS FOR PRODUCTION
: FILE REFERENCE: HBI-0930PC
: CURRENT APPLICATION NUMBER: PCT/US00/07946
: CURRENT FILING DATE: 2000-03-24
: EARLIER APPLICATION NUMBER: 60/126,603
: PRIOR FILING DATE: March 25, 1999
: NUMBER OF SEQ ID NOS: 675
: SOFTWARE: PatentIn Ver. 2.0

```

SEQ ID NO 664
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
PCT-0500-07946-664

Query Match
Best Local Similarity 100.0%; Score 31; DB 1; Length 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 31 SYMS 35

RESULT 7
PCT-0500-07946-666
Sequence 666, Application PC/TUS0007946
GENERAL INFORMATION: Salfield et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BB-093CPC
CURRENT APPLICATION NUMBER: PCT/US00/07946
CURRENT FILING DATE: 2000-03-24
EARLIER FILING DATE: MATCH 25, 1993
HARDWARE: IBM PC compatible
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 666
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
PCT-0500-07946-666

Query Match
Best Local Similarity 100.0%; Score 31; DB 1; Length 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 31 SYMS 35

RESULT 8
US-08-124-469-32
Sequence 32, Application US/08124469
GENERAL INFORMATION: Basell
APPLICANT: BASILL, J. J.
TITLE OF INVENTION: GRAVES' OPHTHALMOPATHY ASSOCIATED
TITLE OF INVENTION: ANTIBODIES, GRAVES' OPHTHALMOPATHY ORBITAL ANTIGEN,
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
STREETS: 1455 PENNSYLVANIA AVE., N.W.
CITY: WASHINGTON,
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: NIXON, HENRY N.
REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 102,105,301
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)942-8400
TELEFAX: (202)942-8484

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-124-469-32

Query Match
Best Local Similarity 100.0%; Score 31; DB 5; Length 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 31 SYMS 35

RESULT 9
US-08-472-771-32
Sequence 32, Application US/08472771
GENERAL INFORMATION:
APPLICANT: RAOPOORT, Basill
APPLICANT: MCLOACHAN, Sandra M.
TITLE OF INVENTION: GRAVES' OPHTHALMOPATHY ASSOCIATED
TITLE OF INVENTION: ANTIBODIES, GRAVES' OPHTHALMOPATHY ORBITAL ANTIGEN,
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
STREETS: 1455 PENNSYLVANIA AVE., N.W.
CITY: WASHINGTON,
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: 08/124,469
FILING DATE: 22-SEP-1993
PROSECUTION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: NIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (202)942-8400
TELEFAX: (202)942-8484
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-771-32

Query Match
Best Local Similarity 100.0%; Score 31; DB 8; Length 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 31 SYMS 35

DB 31 SYMS 35

RESULT 10

US-08-485-202-32

Sequence 32, Application US/08486202

GENERAL INFORMATION:

APPLICANT: RAPPOPORT, Basil

APPLICANT: MCLACHLAN, Sandra M.

TITLE OF INVENTION: GRAVES' OPHTHALMOPATHY ASSOCIATED

NUMBER OF INVENTION: ANTIODIES, GRAVES' OPHTHALMOPATHY ORBITAL ANTIGEN,

CORRESPONDENCE ADDRESS

ADDRESSER: HALE AND DOOR

STREET: 1455 PENNSYLVANIA AVE., N.W.

CITY: WASHINGTON,

STATE: D.C.

COUNTRY: U.S.A.

ZIT: 3000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 05/08/486, 202

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/124,469

FILING DATE: 22-SEP-1993

ATTORNEY/AGENT INFORMATION:

REGISTERED ATTORNEY: HENRY N. 32, 073

REFERENCE/DOCKET NUMBER: 01022105, 301D1Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)942-8400

TELEFAX: (202)942-8484

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-486-202-32

Query Match 100.0%; Score 31; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 31 SYMS 35

Query Match 100.0%; Score 31; DB 8; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-534-717-664

Sequence 664, Application US/09534717

GENERAL INFORMATION:

APPLICANT: SAIGOLD et al

TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

CURRENT APPLICATION NUMBER: US/09/534,717

EARLIER FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/126,603

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-09-534-717-664

Query Match

US-09-534-717-666

Sequence 666, Application US/09534717

GENERAL INFORMATION:

APPLICANT: SAIGOLD et al

APPLICANT: MCLACHLAN, Sandra M.

TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Product

CURRENT APPLICATION NUMBER: US/09/534,717

CURRENT FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/126,603

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-09-534-717-666

Query Match 100.0%; Score 31; DB 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 31 SYMS 35

Query Match 100.0%; Score 31; DB 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-751-181-85

Sequence 181, Application US/09751181

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp

TITLE OF INVENTION: Specific Human Antibodies for Selective Cancer Therapy

CURRENT APPLICATION NUMBER: US/09/751,181

EARLIER FILING DATE: 2000-12-29

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-09-751-181-85

Sequence 181, Application US/09751181

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp

TITLE OF INVENTION: Specific Human Antibodies for Selective Cancer Therapy

CURRENT APPLICATION NUMBER: US/09/751,181

EARLIER FILING DATE: 2000-12-29

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-09-751-181-85

Sequence 181, Application US/09751181

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp

TITLE OF INVENTION: Specific Human Antibodies for Selective Cancer Therapy

CURRENT APPLICATION NUMBER: US/09/751,181

EARLIER FILING DATE: 2000-12-29

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-09-751-181-85

Sequence 181, Application US/09751181

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp

TITLE OF INVENTION: Specific Human Antibodies for Selective Cancer Therapy

CURRENT APPLICATION NUMBER: US/09/751,181

EARLIER FILING DATE: 2000-12-29

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-09-751-181-85

Sequence 181, Application US/09751181

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp

TITLE OF INVENTION: Specific Human Antibodies for Selective Cancer Therapy

CURRENT APPLICATION NUMBER: US/09/751,181

EARLIER FILING DATE: 2000-12-29

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

US-09-751-181-85

Sequence 181, Application US/09751181

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp

TITLE OF INVENTION: Specific Human Antibodies for Selective Cancer Therapy

CURRENT APPLICATION NUMBER: US/09/751,181

EARLIER FILING DATE: 2000-12-29

SEQUENCE CHARACTERISTICS:

LENGTH: 98

TYPE: PRT

ORGANISM: Homo sapiens

```

: TITLE OF INVENTION: Nucleic acids, proteins, and antibodies
: FILE REFERENCE: PM024
: CURRENT APPLICATION NUMBER: US/09/758,455
: CURRENT FILING DATE: 2001-01-11
: PRIOR APPLICATION NUMBER: 60/179,065
: PRIOR FILING DATE: 2000-01-31
: PRIOR APPLICATION NUMBER: 60/180,628
: PRIOR FILING DATE: 2000-02-04
: NUMBER OF SEQ ID NOS: 710
: SOFTWARE: Patentia Ver. 2.0
: SEQ ID NO 598
: LENGTH: 116
: TYPE: PRT
: ORGANISM: Homo sapiens
: PROUNTS: 1
: NAME/REV: SITE
: LOCATION: (115)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-455-598

```

```

Query Match          100.0%; Score 31; DB 21; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 SYMS 5
        |||||
DB      23 SYMS 27

```

```

RESULT 15
US-60-141-701-76
: Sequence 76, Application US/60141701
: GENERAL INFORMATION:
: APPLICANT: Watkins, Bymagic
: TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HIV-1 ENVELOPE
: FILE REFERENCE: 2026-4284
: CURRENT APPLICATION NUMBER: US/60/141,701
: CURRENT FILING DATE: 1999-06-30
: NUMBER OF SEQ ID NOS: 100
: SOFTWARE: Patentia Ver. 2.1
: SEQ ID NO 76
: LENGTH: 123
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus type 1
US-60-141-701-76

```

```

Query Match          100.0%; Score 31; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 SYMS 5
        |||||
DB      32 SYMS 36

```

```

Search completed: November 19, 2001, 08:23:14
Job time: 727 sec

```

THIS PAGE BLANK (USPTO)

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
TYPE: 107
ORGANISM: human
PCT-US01-3234-11

Query Match 87.1%; Score 27; DB 1; Length 107;
Seq. Local Similarity 100.0%; Pred. No. 26;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
DB 32 YWMS 35

RESULT 3
US-09-897-516-6974
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kuehling, Joseph E.
APPLICANT: Kuehling, Joseph E.
APPLICANT: Malver, Thomas W.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
REFERENCE: 38-2151847B
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 6974
TYPE: 107
ORGANISM: Xenorhabdus sp.
US-09-897-516-6974

Query Match 87.1%; Score 27; DB 5; Length 181;
Seq. Local Similarity 100.0%; Pred. No. 41;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
DB 135 YWMS 138

RESULT 4
US-08-721-612C-3
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Evans, Mark J.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Rother, Russell P.
APPLICANT: Matis, Louis A.
TITLE OF INVENTION: Porcine Cell Interaction Proteins
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel, Alexion Pharmaceuticals
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.4MB storage

COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 95
SOFTWARE: PatentIn Ver. 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721.612C
FILING DATE: 26-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004489
FILING DATE: 28-SEPTEMBER-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seth A. Fidel
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
FAX: (203) 772-3655
INFORMATION: 130
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 87.1%; Score 27; DB 4; Length 463;
Seq. Local Similarity 100.0%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWM 4
DB 50 SYWM 53

RESULT 5
US-08-721-612C-9
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Evans, Mark J.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Rother, Russell P.
APPLICANT: Matis, Louis A.
TITLE OF INVENTION: Porcine Cell Interaction Proteins
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel, Alexion Pharmaceuticals
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.4MB storage
OPERATING SYSTEM: Windows 95
SOFTWARE: MICROSOFT WORD 97 SR-2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721.612C
FILING DATE: 26-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004489
FILING DATE: 28-SEPTEMBER-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790

1 TITLE OF INVENTION: Btels
2 FILE REFERENCE: 0208/01254-US0
3 CURRENT APPLICATION NUMBER: US/09/786,039
4 CURRENT FILING DATE: 1999-08-30
5 PRIOR APPLICATION NUMBER: NZ 31612
6 PRIOR FILING DATE: 1999-08-28
7 NUMBER OF SEQ ID NOS: 25
8 SOFTWARE: PASTSEQ for Windows Version 3.0
9 SEQ ID NO 5
10 LENGTH: 255
11 TYPE: PRT
12 ORGANISM: Brevine
13 US-09-786-039-5

Query Match 80.6%; Score 25; DB 5; Length 255;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 44 SYMS 48

RESULT 10
US-60-325-537-24
1 Sequence 24, Application US/60325537
2 GENERAL INFORMATION:
3 APPLICANT: Stein, Joshua C
4 TITLE OF INVENTION: Methods for Analyzing Biological Elements
5 FILE REFERENCE: 16517,246/38-10(52045)A
6 CURRENT APPLICATION NUMBER: US/60/325,537
7 CURRENT FILING DATE: 2000-10-01
8 NUMBER OF SEQ ID NOS: 40
9 SOFTWARE: PatentIn Version 3.1
10 SEQ ID NO 24
11 LENGTH: 324
12 TYPE: PRT
13 ORGANISM: Arabidopsis thaliana
14 US-60-325-537-24

Query Match 80.6%; Score 25; DB 6; Length 324;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 240 SYMS 244

RESULT 11
US-09-815-242-5719
1 Sequence 5719, Application US/09815242
2 GENERAL INFORMATION:
3 APPLICANT: Haselbeck, Robert
4 APPLICANT: Ohlson, Karl L.
5 APPLICANT: Zyskind, Judith W.
6 APPLICANT: Wall, Daniel
7 APPLICANT: Yaskin, John D.
8 APPLICANT: Carr, Grant J.
9 APPLICANT: Yamamoto, Robert T.
10 APPLICANT: Xu, H. Howard
11 TITLE OF INVENTION: Identification of Essential Genes in
12 Prokaryotes
13 REFERENCE: ELTRA-01A
14 CURRENT APPLICATION NUMBER: US/09/815,242
15 PRIOR FILING DATE: 2000-03-21
16 PRIOR APPLICATION NUMBER: 60/151,078
17 PRIOR FILING DATE: 2000-03-21
18 PRIOR APPLICATION NUMBER: 60/206,848
19 PRIOR FILING DATE: 2000-05-23

1 PRIOR APPLICATION NUMBER: 60/207,727
2 PRIOR FILING DATE: 2000-05-26
3 PRIOR APPLICATION NUMBER: 60/242,578
4 PRIOR FILING DATE: 2000-10-21
5 PRIOR APPLICATION NUMBER: 60/255,625
6 PRIOR FILING DATE: 2000-11-27
7 PRIOR APPLICATION NUMBER: 60/257,931
8 PRIOR FILING DATE: 2000-12-22
9 PRIOR APPLICATION NUMBER: 60/269,308
10 PRIOR FILING DATE: 2001-02-16
11 NUMBER OF SEQ ID NOS: 14110
12 SOFTWARE: PASTSEQ for Windows Version 4.0
13 SEQ ID NO 5719
14 LENGTH: 478
15 TYPE: PRT
16 ORGANISM: Staphylococcus aureus
17 US-09-815-242-5719

Query Match 80.6%; Score 25; DB 5; Length 478;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5
DB 169 SYMS 173

RESULT 12
US-09-815-242-12480
1 Sequence 12480, Application US/09815242
2 GENERAL INFORMATION:
3 APPLICANT: Haselbeck, Robert
4 APPLICANT: Ohlson, Karl L.
5 APPLICANT: Zyskind, Judith W.
6 APPLICANT: Wall, Daniel
7 APPLICANT: Yaskin, John D.
8 APPLICANT: Carr, Grant J.
9 APPLICANT: Yamamoto, Robert T.
10 APPLICANT: Xu, H. Howard
11 TITLE OF INVENTION: Identification of Essential Genes in
12 Prokaryotes
13 REFERENCE: ELTRA-01A
14 CURRENT APPLICATION NUMBER: US/09/815,242
15 PRIOR FILING DATE: 2000-03-21
16 PRIOR APPLICATION NUMBER: 60/151,078
17 PRIOR FILING DATE: 2000-03-21
18 PRIOR APPLICATION NUMBER: 60/206,848
19 PRIOR FILING DATE: 2000-05-23
20 PRIOR APPLICATION NUMBER: 60/207,727
21 PRIOR FILING DATE: 2000-05-26
22 PRIOR APPLICATION NUMBER: 60/242,578
23 PRIOR FILING DATE: 2000-10-23
24 PRIOR APPLICATION NUMBER: 60/253,625
25 PRIOR FILING DATE: 2000-11-27
26 PRIOR APPLICATION NUMBER: 60/257,931
27 PRIOR FILING DATE: 2000-12-22
28 PRIOR APPLICATION NUMBER: 60/269,308
29 PRIOR FILING DATE: 2001-02-16
30 NUMBER OF SEQ ID NOS: 14110
31 SOFTWARE: PASTSEQ for Windows Version 4.0
32 SEQ ID NO 12480
33 LENGTH: 478
34 TYPE: PRT
35 ORGANISM: Staphylococcus aureus
36 US-09-815-242-12480

Query Match 80.6%; Score 25; DB 5; Length 478;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMS 5

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:11:07 : Search time 43.5 Seconds
(without alignments)

2.587 Million cell updates/sec

Title: US-09-610-118-61

Perfect score: 31

Sequence: 1 SYMS 5

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2.6/p/odata/2/1aa/5k.COMB.pep.*
2: /cgn2.6/p/odata/2/1aa/5k.COMB.pep.*
3: /cgn2.6/p/odata/2/1aa/6k.COMB.pep.*
4: /cgn2.6/p/odata/2/1aa/8k.COMB.pep.*
5: /cgn2.6/p/odata/2/1aa/10k.COMB.pep.*
6: /cgn2.6/p/odata/2/1aa/backlist.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	98	1	US-07-942-245-37
2	31	100.0	117	3	US-08-542-809A-95
3	28	90.3	5	2	US-08-318-82B-43
4	28	90.3	10	1	US-08-208-886C-87
5	28	90.3	10	1	US-08-704-744-85
6	28	90.3	10	1	US-08-704-744-89
7	28	90.3	10	1	US-08-469-557-64
8	28	90.3	10	1	US-08-469-557-68
9	28	90.3	10	2	US-08-290-732B-64
10	28	90.3	10	2	US-08-290-732B-68
11	28	90.3	118	3	US-08-767-128-6
12	28	90.3	118	3	US-08-767-128-6
13	28	90.3	119	2	US-08-318-157B-2
14	28	90.3	119	2	US-08-318-157B-8
15	28	90.3	119	2	US-08-318-157B-9
16	28	90.3	119	2	US-08-318-157B-10
17	28	90.3	119	2	US-08-318-157B-11
18	28	90.3	119	2	US-08-318-157B-12
19	28	90.3	119	2	US-08-318-157B-13
20	28	90.3	119	2	US-08-318-157B-14
21	28	90.3	119	2	US-08-318-157B-15
22	28	90.3	119	2	US-08-318-157B-16
23	28	90.3	119	2	US-08-318-157B-17
24	28	90.3	119	2	US-08-318-157B-18
25	28	90.3	119	2	US-08-318-157B-19
26	28	90.3	119	2	US-08-318-157B-20
27	28	90.3	218	2	US-08-359-889-25

28	28	90.3	218	3	US-09-167-364-25	Sequence 25, Appl
29	28	90.3	218	4	US-08-439-897-4	Sequence 11, Appl
30	28	90.3	241	1	US-08-445-478B-11	Sequence 11, Appl
31	28	90.3	298	4	US-09-318-661-2	Sequence 2, Appl
32	28	90.3	467	1	US-08-704-744-81	Sequence 81, Appl
33	28	90.3	471	2	US-08-399-889-24	Sequence 24, Appl
34	28	90.3	471	2	US-08-399-889-24	Sequence 24, Appl
35	28	90.3	471	3	US-09-167-364-24	Sequence 2, Appl
36	28	90.3	471	4	US-09-439-897-2	Sequence 16, Appl
37	28	90.3	503	3	US-08-700-858-16	Sequence 16, Appl
38	28	90.3	503	3	US-08-700-858-16	Sequence 16, Appl
39	28	90.3	637	2	US-08-445-478B-15	Sequence 15, Appl
40	28	90.3	696	1	US-08-765-081-5	Sequence 5, Appl
41	28	90.3	696	3	US-09-098-082-5	Sequence 5, Appl
42	28	90.3	696	5	PCT-US95-06994-8	Sequence 5, Appl
43	28	90.3	703	5	PCT-US95-06994-8	Sequence 5, Appl
44	28	90.3	718	1	PCT-US95-06994-6	Sequence 2, Appl
45	28	90.3	1694	1	US-08-434-108-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-942-245-37
Sequence 37, Application US-0794245
PCT-US95-06994-6
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
INVENTOR: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
INVENTOR: SEARLE, Stephen M.J.
APPLICANT: ROGERS, Michael A.
INVENTOR: ROGERS, Michael A.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughree, Mlou, Zlim, Caspach & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 5000/700 workstation
OPERATING SYSTEM: UNIX
CURRENT APPLICATION DATA:
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: Peptide
US-07-942-245-37

Query Match 100.0%; Score 31; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

DB 31 SYMS 35

RESULT 2
US-08-318-1578-95
Sequence 23, Application US/08345809A
Patent No. 5696678
GENERAL INFORMATION:
APPLICANT: Honjo, Takanu
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
CLASSIFICATION: C07K 231.13
NAMES: Honjo, Takanu, Matsuda, Fumihiko
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545.809A
FILING DATE: 10-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
ADDRESS: 1000 West 12th Street, 29.066
REFERENCE/DOCKET NUMBER: 32.364
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INVENTION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-345-809A-95

Query Match 100.0%; Score 31; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYMS 5
111111
DB 50 SYMS 54

RESULT 3
US-08-318-1578-23
Sequence 23, Application US/083181578
Patent No. 5874340
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
APPLICANT: ARMOUR, Kathryn L.
TITLE OF INVENTION: CAR-GRAFTED TYPE III ANTI-CEA HUMANIZED
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1000 West 12th Street, Suite 500
STREET: 1000 West 12th Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318.1578
FILING DATE: 05-OCT-1994
CLASSIFICATION: C07K 231.13
NAMES: Saxe, Bernhard D.
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28.665
REFERENCE/DOCKET NUMBER: 1873/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/672-5300
TELEFAX: 202/672-5399
TELEX: 904116
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-1578-23

Query Match 90.3%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 16e05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYMS 5
111111
DB 1 SYMS 5

RESULT 4
US-08-208-886C-83
Sequence 83, Application US/08208886C
Patent No. 5597710
GENERAL INFORMATION:
APPLICANT: Daille, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: HANSEN, Hans J.
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 1000 Clipping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208.886C
FILING DATE: March 10, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32.364
REFERENCE/DOCKET NUMBER: JB0429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908.295.5387
TELEFAX: 908.295.5386
INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-208-886C-83

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 25;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMMS 5
|||||
DB 6 SYMWT 10

RESULT 5
US-08-208-886C-87
Sequence 87, Application US/0820886C
PATENT No. 5597710
GENERAL INFORMATION:
APPLICANT: Daille, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA: US/08/208,886C
FILING DATE: March 10, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ROUTE, Cynthia L.
ADDRESS: 1000 Route 132, 364
REFERENCE/DOCKET NUMBER: J80429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 2987
TELEFAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-208-886C-87

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 25;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMMS 5
|||||
DB 6 SYMWT 10

RESULT 6

US-08-704-744-85
Sequence 85, Application US/08704744

PATENT No. 5705134
GENERAL INFORMATION:
APPLICANT: Daille, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA: US/08/704,744
FILING DATE: 08-MAR-1995
APPLICATION NUMBER: 08-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: ROUTE, Cynthia L.
ADDRESS: 1000 Route 132, 364
REFERENCE/DOCKET NUMBER: J80429K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-744-85

Query Match 90.3%; Score 28; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 25;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMMS 5
|||||
DB 6 SYMWT 10

RESULT 7
US-08-704-744-89
Sequence 89, Application US/08704744
PATENT No. 5705134
GENERAL INFORMATION:
APPLICANT: Daille, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey

COUNTRY: USA
 ZIP: 07033-0530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: APPLE Macintosh
 SOFTWARE: Microsoft Word 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/704,744
 FILING DATE: 06-SEPT-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/208886
 FILING DATE: 10-MAR-1994
 APPLICATION NUMBER: PCT/US/95/02400
 FILING DATE: 08-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Foulke, Cynthia L.
 REGISTRATION NUMBER: 32,364
 REFERENCE/DOCKET NUMBER: 240947
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 298-2987
 TELEFAX: (908) 298-5388
 TELEX:
 IMPORTANT FOR SEQ ID NO: 89:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-704-744-89

Query Match 90.3%; Score 28; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 25
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SYMS 5
 Db 6 SYMT 10

RESULT 8
 US-08-469-557-64
 Sequence 64, Application US/08469557
 GENERAL INFORMATION:
 PATENT NO. 5770403
 APPLICANT: Daiile, Barbara
 APPLICANT: Le, Hung
 APPLICANT: Muller, Kenneth
 APPLICANT: Murgolo, Nicholas
 APPLICANT: Nguyen, Hanh
 APPLICANT: Tindall, Stephen
 TITLE OF INVENTION: Cloning and Expression of
 TITLE OF INVENTION: Humanized Monoclonal Antibodies
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Schering-Plough Corporation
 STREET: 2000 Gallotopg Hill Road
 CITY: Kenilworth
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07033-0530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: APPLE Macintosh
 SOFTWARE: Microsoft Word 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,557
 FILING DATE: 06-JUN-1995

CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/290,793
 FILING DATE: August 16, 1994
 APPLICATION NUMBER: PCT/US93/01301
 FILING DATE: 19-FEB-1992
 APPLICATION NUMBER: US 07/841,659
 FILING DATE: 19-FEB-1992
 APPLICATION NUMBER: US 07/82,784
 FILING DATE: 24-OCT-1991
 APPLICATION NUMBER: US 07/499,327
 FILING DATE: 21-MAY-1990
 APPLICATION NUMBER: PCT/US88/03631
 FILING DATE: 21-OCT-1988
 APPLICATION NUMBER: US 07/655,966
 FILING DATE: 26-OCT-1987
 APPLICATION NUMBER: US 06/881,553
 FILING DATE: 03-JUL-1986
 APPLICATION NUMBER: US 06/843,958
 FILING DATE: 25-MAR-1986
 APPLICATION NUMBER: US 06/799,668
 FILING DATE: 19-NOV-1985
 ATTORNEY/AGENT INFORMATION:
 NAME: Foulke, Cynthia L.
 REGISTRATION NUMBER: 32,364
 REFERENCE/DOCKET NUMBER: 240947
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 298-2987
 TELEFAX: 908-298-5388
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-469-557-64

Query Match 90.3%; Score 28; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 25;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 Oy 1 SYMS 5
 Db 6 SYMT 10

RESULT 9
 US-08-469-557-68
 Sequence 68, Application US/08469557
 Patent No. 5770403
 GENERAL INFORMATION:
 APPLICANT: Daiile, Barbara
 APPLICANT: Le, Hung
 APPLICANT: Muller, Kenneth
 APPLICANT: Murgolo, Nicholas
 APPLICANT: Nguyen, Hanh
 APPLICANT: Tindall, Stephen
 APPLICANT: Zavodny, Paul
 TITLE OF INVENTION: Cloning and Expression of
 TITLE OF INVENTION: Humanized Monoclonal Antibodies
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Schering-Plough Corporation
 STREET: 2000 Gallotopg Hill Road
 CITY: Kenilworth
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07033-0530
 COMPUTER READABLE FORM:


```

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,557
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,793
FILING DATE: August 16, 1994
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/782,784
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: US 07/499,327
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 06/843,958
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/655,966
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: US 07/113,623
FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/881,553
FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 37,364
REFERENCE/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
STRANDNESS: acid
TOPOLOGY: linear
US-08-469-557-68

Query Match          90.3%  Score 28; DB 1; Length 10;
Best Local Similarity 80.0%  Pred. No. 25;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SYMS 5
||||:
DB 6 SYMT 10

```

```

RESULT 10
US-08-290-793B-64
Sequence 64, Application US/08290793B
Patent No. 5863537
GENERAL INFORMATION:
APPLICANT: Dalle, Barbara
APPLICANT: Le, Hung Kenneth
APPLICANT: Miller, Nicholas
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin 4
INVENTOR: Zavodny, Paul
CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Schering-Plough Corporation
STREET: 1400 South Plough Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,793B
FILING DATE: August 16, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/782,784
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: US 07/499,327
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: PCT/US88/03631
FILING DATE: 21-OCT-1987
APPLICATION NUMBER: US 07/655,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/113,623
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: US 06/881,553
FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 37,364
REFERENCE/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
US-08-290-793B-64

Query Match          90.3%  Score 28; DB 2; Length 10;
Best Local Similarity 80.0%  Pred. No. 25;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SYMS 5
||||:
DB 6 SYMT 10

```

```

RESULT 11
US-08-290-793B-68
Sequence 68, Application US/08290793B
Patent No. 5863537
GENERAL INFORMATION:
APPLICANT: Dalle, Barbara
APPLICANT: Le, Hung Kenneth
APPLICANT: Miller, Nicholas
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Cloning and Expression of

```

TITLE OF INVENTION: Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin-4
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS: Biontech Corporation
ADDRESS: 1415 Central Expressway
CITY: Kailua
STREET: 2000 Kailua Road
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,793B
PRIORITY DATE: August 16, 1994
PRIORITY NUMBER: PCT/US93/01301
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/782,784
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: US 07/499,327
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: PCT/US88/03631
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: US 07/555,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/113,623
FILING DATE: 22-OCT-1987
APPLICATION NUMBER: US 06/881,553
FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
PRIORITY DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 37,364
REFERENCE/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-290-793B-68

Query Match 90.3% Score 28; DB 2; Length 10;
Best Local Similarity 80.0% Pred. No. 25;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYNM 5
|||||
DB 6 SYNM 10

RESULT 12
US-08-767-128-2
Sequence 2, Application US/08/67128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLLIE, DMANE E.
* APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER

TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFOR
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant, Gould, Smith, Ball, Melter & Schmidt
STREET: 3100 No. 611079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 42C-1996
CLASSIFICATION: 42C-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 07-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 2409S71
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGIN: Internal
ORIGINAL SOURCE:
US-08-767-128-2

Query Match 90.3% Score 28; DB 3; Length 118;
Best Local Similarity 80.0% Pred. No. 2,2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYNM 5
|||||
DB 31 SYNM 35

RESULT 13
US-08-767-128-8
Sequence 8, Application US/08/67128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLLIE, DMANE E.
* APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER JOSEPH
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND

TELEFAX: (202)672-5399
 TELE: 504136
 INFORMATION FOR SEQ ID NO: 8:
 SOURCE: SCIENCE CHARACTERISTICS:
 FUNCTION: amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-318-157B-8

Query Match 90.38; Score 28; DB 2; Length 119;
 Best Local Similarity 80.08; Pred. No. 2,2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STWMS 5
 : : : : :
 Db 31 TWMS 35

Search completed: November 19, 2001, 08:13:24
 Job time: 137 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM Protein - protein search, using sw model

Run on: November 19, 2001, 08:14:20 : Search time 48.99 seconds

(without alignments) 26.433 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89 NIKOSSEKRYADSVAG 17

Sequence: BIOSUM62

Scoring table: Gapex 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database: PIR.68:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	86	96.6	147	2	I37780
2	82	92.1	97	2	I37780
3	82	92.1	98	2	PI0123
4	82	92.1	110	2	PI1555
5	82	92.1	114	2	S36280
6	82	92.1	117	2	S17025
7	82	92.1	122	2	S31675
8	82	92.1	136	2	S31687
9	82	92.1	139	2	I37781
10	82	92.1	140	2	S22657
11	79	88.8	142	2	S31509
12	77	86.5	133	2	S31509
13	77	86.5	136	2	S31509
14	67	72.3	136	2	S60294
15	66	74.2	98	2	S29543
16	66	74.2	117	2	S36259
17	66	74.2	134	2	S31688
18	66	74.2	135	2	S31598
19	66	74.2	140	2	S70442
20	65	73.0	141	2	PI0120
21	64	71.9	97	2	S44115
22	64	71.9	98	2	PI0116
23	64	71.9	98	2	S29546
24	64	71.9	109	2	PI1644
25	64	71.9	109	2	PI1646
26	64	71.9	111	2	PI1645
27	64	71.9	111	2	PI1645
28	64	71.9	113	2	S38490

ALIGNMENTS

30	64	71.9	114	2	S46390	19	heavy chain V F
31	64	71.9	114	2	S46392	19	heavy chain V F
32	64	71.9	117	2	S36270	19	heavy chain V F
33	64	71.9	118	2	S31116	19	heavy chain V F
34	64	71.9	119	2	S36005	19	heavy chain V F
35	64	71.9	120	2	S31112	19	heavy chain V F
36	64	71.9	121	2	S19656	19	heavy chain V F
37	64	71.9	121	2	S36005	19	heavy chain V F
38	64	71.9	122	2	S36005	19	heavy chain V F
39	64	71.9	122	2	S36005	19	heavy chain V F
40	64	71.9	122	2	S38493	19	heavy chain V F
41	64	71.9	130	2	PI0098	19	heavy chain V F
42	64	71.9	133	2	S31603	19	heavy chain V F
43	64	71.9	134	2	S31679	19	heavy chain V F
44	64	71.9	139	2	S31674	19	heavy chain V F
45	64	71.9	139	2	S31674	19	heavy chain V F

RESULT 1

I37780
IG variable region (VDJ) (clone 720-11) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-19780, revision 16-Feb-1996 #text_change 23-Jul-1999
R:Domain: C: Chastagner, P.; These, J.; Xouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed b
A:Reference number: A36876; MID:94119917
A:Accession: I37780
A:Status: preliminary
A:Residues: 1-147 (KRS>
A:Cross-references: EMBL: X67943; MID:933578; PIDN:CAA48130.1; PID:933579
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:28-11/Domain: Immunoglobulin homology <IMV>

Query Match

Best Local Similarity 96.6% Score 86; DB 2; Length 147;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIKOSSEKRYADSVAG 17
DB 63 NIKOSSEKRYADSVAG 79

RESULT 2

PH0872
IG heavy chain V region (anti-DNA, IIT-3R) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence-revision 09-Oct-1992 #text_change 16-Aug-1996
A:Accession: PH0872
J Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A:Reference number: PH0862; MID:92078875
A:Accession: PH0872
A:Molecule type: DNA
A:Residues: 1-147 (KRS>
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:14-97/Domain: Immunoglobulin homology <IMV>
F:30-35/Region: complementarity-determining 1
F:49-66/Region: complementarity-determining 2

Query Match 92.1% Score 82; DB 2; Length 97;
Best Local Similarity 88.2% Pred. No. 1.1e-05;

Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKODSEKRYADSVAG 17
|||||
Db 49 NIKODSEKRYADSVAG 65

RESULT 3

19 heavy chain V-II region (TD-Vr) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence-revision 07-Jun-1990 #text-change 23-Jul-1999
C:Accession: P01023; S26897
R:Bird, J.; Galili, N.; Link, M.; Scites, D.; Sklar, J.
A:Title: Control of V(D)J recombination but absence of somatic hypermutation in immunoglobulin
A:Reference number: P01016; MUID:8626005
A:Accession: P01023
A:Molecule type: mRNA
A:Residues: 1-98 <R19>
A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia. All
A:Accession: S26897
A:Accession: S26897
B:Tomlinson, S.; Marks, J.D.; Livey, M.B.; Wilter, G.
J. Mol. Biol. 227: 776-786, 1992
A:Title: The repertoire of human germline VH sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:9302117
A:Accession: S26897
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <R19>
A:Cross-references: EMBL:212354; NID:932930; RDN:CAV8224.1; PID:932931
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IHW>
F:19-65/region: complementarity-determining 2

Query Match

Best Local Similarity 92.1%; Score 82; DB 2; Length 98;
Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKODSEKRYADSVAG 17
|||||
Db 50 NIKODSEKRYADSVAG 66

RESULT 4

19 heavy chain V region (clone 2B8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence-revision 24-Feb-1994 #text-change 16-Aug-1996
R:Hillison, J.L.; Kerr, N.S.; Oppliger, I.R.; Monnik, M.; Sasso, E.H.
J. Exp. Med. 178: 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Accession number: P01642; MUID:93301610
A:Molecule type: RNA
A:Residues: 1-110 <R15>
A:Experimental source: B cell
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:17-90/Domain: Immunoglobulin homology <IHW>

Query Match

Best Local Similarity 92.1%; Score 82; DB 2; Length 110;
Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKODSEKRYADSVAG 17
|||||
Db 42 NIKODSEKRYADSVAG 58

RESULT 5

19 heavy chain V region (clone alpha-P01-A3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Feb-1994 #sequence-revision 03-Feb-1994 #text-change 17-Mar-1999
R:Griffiths, A.D.; Maloney, M.; Marks, J.D.; Bye, J.M.; Amberton, M.J.; McCafferty, J.
EMBO J. 12: 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display library
A:Reference number: S36256; MUID:93178448
A:Accession: S36280
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-114 <R15>
A:Cross-references: EMBL:218822
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IHW>

Query Match

Best Local Similarity 92.1%; Score 82; DB 2; Length 114;
Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKODSEKRYADSVAG 17
|||||
Db 50 NIKODSEKRYADSVAG 66

RESULT 6

19 heavy chain V region (clone FLJ3-28) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-May-1998 #sequence-revision 08-May-1998 #text-change 21-Jan-2000
R:Raaphorst, F.M.; S1115
submitted to the EMBL data library, October 1991
A:Reference number: S78486
A:Accession: S78486
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <R15>
A:Cross-references: EMBL:X6965
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schur
Eur. J. Immunol. 22: 247-251, 1992
A:Title: Restricted utilization of germ-line VH3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633
A:Accession: S31113
A:Molecule type: RNA
A:Residues: 1-63, 'G', 34-52, 'E', 54-73, 'K', 75-97 <R15>
A:Cross-references: EMBL:X6965
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IHW>

Query Match

Best Local Similarity 92.1%; Score 82; DB 2; Length 117;
Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIKODSEKRYADSVAG 17
|||||
Db 50 NIKODSEKRYADSVAG 66

RESULT 7

19 heavy chain V-gene (clone HHC19) - human
C:Species: Homo sapiens (man)
C:Date: 07-Feb-1995 #sequence-revision 20-Feb-1995 #text-change 23-Jul-1999
C:Accession: S60293; S17075

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S31509
 R:Chastagner, P.; Demalson, C.; Theze, J.; Togni, M.
 submitted to the EMBL Data Library, December 1992
 A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
 A:Reference number: S31509
 A:Accession: S31509
 A:Species: Homo sapiens (man)
 A:Molecule: 1:123 <RNA>
 A:Residues: 1-123
 A:Cross-references: EMBL:X69864; NID:933090; PTDN:CA46498.1; PTD:933091
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 86.5%; Score 77; DB 2; Length 123;
 Best Local Similarity 82.4%; Pred. No. 1e-05;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 IKQDSERYADSVRG 17
 DB 58 NIKDSERYADSVRG 74

RESULT 13
 S16847
 19 heavy chain V region - human
 C:Accession: Homo sapiens (man)
 C>Date: 20-Jan-1993 #sequence_revision 20-Feb-1995 #text_change 16-Aug-1996
 C:Accession: S16847
 R:Knappert, R.
 submitted to the EMBL Data Library, September 1991
 A:Reference number: S16847
 A:Accession: S16847
 A:Species: Homo sapiens (man)
 A:Molecule: 1:136 <RNA>
 A:Residues: 1-136
 A:Cross-references: EMBL:X62126
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 75.3%; Score 67; DB 2; Length 136;
 Best Local Similarity 68.8%; Pred. No. 0.00055;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 IKQDSERYADSVRG 17
 DB 70 VKQDSERYADSVRG 85

RESULT 14
 S60296
 19 heavy-chain variable region (clone WMR) precursor - human (fragment)
 C:Accession: Homo sapiens (man)
 C>Date: 20-Jan-1993 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000
 C:Accession: S60296
 R:Knappert, R.; Fischer, U.; Rajewsky, K.; Gause, A.
 Immunol. Lett. 34, 57-67, 1992
 A:Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive Imm
 A:Reference number: S60295; MUID:93122853
 A:Accession: S60296
 A:Species: Homo sapiens (man)
 A:Molecule type: DNA
 A:Residues: 1-136 <RNA>
 A:Cross-references: EMBL:X62126; NID:938336; PTDN:CA44057.1; PTD:938337
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match

75.3%; Score 67; DB 2; Length 136;

Best Local Similarity 68.8%; Pred. No. 0.00055;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 IKQDSERYADSVRG 17
 DB 70 VKQDSERYADSVRG 85

RESULT 15
 S29543
 19 heavy chain V region (COS 3) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S29543
 R:Knappert, R.; Fischer, U.; Rajewsky, K.; Gause, A.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S29543
 A:Accession: S29543
 A:Molecule type: DNA
 A:Residues: 1-98 <RNA>
 A:Cross-references: EMBL:X217389; NID:932835; PTDN:CA478994.1; PTD:932836
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; Immunoglobulin
 F:15-96/Domain: Immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 98;
 Best Local Similarity 75.0%; Pred. No. 0.00057;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 IKQDSERYADSVRG 17
 DB 51 IRQDSERYADSVRG 66

Search completed: November 19, 2001, 08:14:20
 Job time: 193 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:25:33 : Search time 27.32 Seconds
(without alignments)
21.316 Million cell updates/sec

Title: US-09-610-118-62

Database: 1 NIKOSSEXYADSVRG 17

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapex 0.5

Searched: 93435 seqs, 3425466 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	70.8	116	HV37_HUMAN	homo sapien
2	57	64.0	112	HV37_HUMAN	homo sapien
3	56	64.0	112	HV37_HUMAN	homo sapien
4	55	61.8	119	HV31_HUMAN	homo sapien
5	55	61.8	119	HV31_HUMAN	homo sapien
6	55	61.8	119	HV31_HUMAN	homo sapien
7	50	56.2	119	HV31_HUMAN	homo sapien
8	49	55.1	119	HV31_HUMAN	homo sapien
9	47	52.8	122	HV31_HUMAN	homo sapien
10	47	52.8	122	HV31_HUMAN	homo sapien
11	46	51.7	117	HV31_HUMAN	homo sapien
12	46	51.7	117	HV31_HUMAN	homo sapien
13	46	51.7	117	HV31_HUMAN	homo sapien
14	45	50.6	98	HV57_HUMAN	homo sapien
15	45	50.6	98	HV57_HUMAN	homo sapien
16	44	49.4	115	HV31_HUMAN	homo sapien
17	44	49.4	115	HV31_HUMAN	homo sapien
18	44	49.4	115	HV31_HUMAN	homo sapien
19	43	48.3	110	HV31_HUMAN	homo sapien
20	42	47.2	117	HV31_HUMAN	homo sapien
21	42	47.2	117	HV31_HUMAN	homo sapien
22	41	46.1	117	HV01_CACOR	homo sapien
23	41	46.1	117	HV01_CACOR	homo sapien
24	41	46.1	117	HV01_CACOR	homo sapien
25	40	44.9	117	HV54_MOUSE	mus musculus
26	40	44.9	117	HV54_MOUSE	mus musculus
27	40	44.9	117	HV54_MOUSE	mus musculus
28	40	44.9	117	HV54_MOUSE	mus musculus
29	40	44.9	117	HV54_MOUSE	mus musculus
30	40	44.9	117	HV54_MOUSE	mus musculus
31	40	44.9	117	HV54_MOUSE	mus musculus
32	39	43.8	117	HV51_MOUSE	mus musculus
33	39	43.8	117	HV51_MOUSE	mus musculus

34	39	43.8	178	V319_ARCSE	P47561 MYOGLIUM
35	39	43.8	178	V319_ARCSE	P47561 MYOGLIUM
36	39	43.8	178	V319_ARCSE	P47561 MYOGLIUM
37	39	43.8	178	V319_ARCSE	P47561 MYOGLIUM
38	39	43.8	178	V319_ARCSE	P47561 MYOGLIUM
39	39	43.8	178	V319_ARCSE	P47561 MYOGLIUM
40	39	43.8	178	V319_ARCSE	P47561 MYOGLIUM
41	39	43.8	178	V319_ARCSE	P47561 MYOGLIUM
42	38.5	43.3	177	V319_ARCSE	P47561 MYOGLIUM
43	38	42.7	149	V319_ARCSE	P47561 MYOGLIUM
44	38	42.7	149	V319_ARCSE	P47561 MYOGLIUM
45	38	42.7	159	V319_ARCSE	P47561 MYOGLIUM

ALIGNMENTS

RESULT	1	STANDARD	PRT	116 AA.
AC HV37_HUMAN				
AD P01781:				
DT 21-JUL-1986 (Rel. 01, Created)				
DT 21-JUL-1986 (Rel. 01, Last sequence update)				
DE 15-JUL-1999 (Rel. 38, Last annotation update)				
DE HEAVY CHAIN V-III REGION GNL.				
OS Homo sapiens (human)				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.				
NCBI_Taxid=9606;				
1				
2				
3				
4				
5				
6				
7				
8				
9				
10				
11				
12				
13				
14				
15				
16				
17				
18				
19				
20				
21				
22				
23				
24				
25				
26				
27				
28				
29				
30				
31				
32				
33				
34				
35				
36				
37				
38				
39				
40				
41				
42				
43				
44				
45				

Query Match	70.8%	Score 63	DB 1	Length 116
Best Local Similarity	58.8%	Pred. No. 0.0005		
Matches 10	Conservative	5	Mismatches 2	Indels 0
0				
1	NIKOSSEXYADSVRG 17			
DB	50 NIKOSSEXYADSVRG 66			
RESULT				
AC HV37_HUMAN				
AD P01781:				
DT 21-JUL-1986 (Rel. 01, Created)				
DT 21-JUL-1986 (Rel. 01, Last sequence update)				
DE 15-JUL-1999 (Rel. 38, Last annotation update)				
DE HEAVY CHAIN V-III REGION CAM.				
OS Homo sapiens (human)				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.				
NCBI_Taxid=9606;				

RM 111
 SEQUENCE: PubMed:6774332;
 RX MEDLINE:6774332;
 RA Lehman D.W. Putnam
 RT Amino acid sequence of the variable region of a human mu chain:
 RL location of a possible JH segment.
 CC Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
 PIR: PATIENT WITH MACROGLOBULINEMIA.
 DR HSSP: P01772.2102CM.
 DR InterPro: IPR003006.
 DR Pfam: PF00047.19.1.
 KW Immunoglobulin V region.
 RM MOD_RES 122 122
 FT MOD_RES 122 122
 FT SEQUENCE 122 AA; 13668 MW; M42D0F17D25F1C2 CRC64;

Query Match 64.0%; Score 57; DB 1; Length 122;
 Best Local Similarity 56.2%; Pred. No. 0.0056;
 Matches 9: Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKDGSERYVADSVRG 17
 DB 51 ISTDGSRVYADSVRG 66

RESULT 3
 HV3K_HUMAN STANDARD; PRT; 118 AA.
 AC P01772.1
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION GAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_TaxID:9606;
 RP SEQUENCE.
 RA MEDLINE:9525298; PubMed:7737190;
 RA Schoppa M., Bellotti V., Negri G., Garver F., Ferris G.;
 RT Characterization of the two unique human anti-flavin monoclonal
 RL Eur. J. Biochem. 228:886-893(1995).
 DR HSSP: P01810.2PM7.
 DR InterPro: IPR003006.
 DR Pfam: PF00047.19.1.
 KW Immunoglobulin V region.
 RM MOD_RES 118 118
 FT MOD_RES 118 118
 FT SEQUENCE 118 AA; 13087 MW; 6C21D810ED1BED1F CRC64;

Query Match 63.9%; Score 56; DB 1; Length 118;
 Best Local Similarity 62.5%; Pred. No. 0.0053;
 Matches 10: Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 IKDGSERYVADSVRG 16
 DB 50 NIDPDETFYSISVA 65
 RESULT 4
 HV3L_HUMAN STANDARD; PRT; 119 AA.
 AC P01773.1
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION BUR.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_TaxID:9606;
 RP SEQUENCE (WYELONA PROTEIN BUR).
 RX MEDLINE:79151016; PubMed:107164;
 RA Pullum F.W., Liu Y.-S.V., Low T.L.K.;
 RT Primary structure of a human IgM1 immunoglobulin, IV. Streptococcal
 RT IgM1 antibody structure of the Fab and Fc fragments, and the complete
 RT amino acid sequence of the heavy chain.
 DR J. Biol. Chem. 254:2865-2874(1979).
 DR PIR: A02056; A1HUBR.
 DR HSSP: P01772.2102.
 DR InterPro: IPR003006.
 DR Pfam: PF00047.19.1.
 KW Immunoglobulin V region: glycoprotein.
 RM MOD_RES 122 96
 FT MOD_RES 122 96
 FT DISULFID 22 28
 FT CARBOHYD 28 28
 FT NON_TER 119 119
 FT SEQUENCE 119 AA; 12981 MW; 12A709A7344D024 CRC64;

Query Match 61.8%; Score 55; DB 1; Length 119;
 Best Local Similarity 60.8%; Pred. No. 0.013; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKDGSERYVADSVRG 17
 DB 51 ISTDGSRVYADSVRG 66

RESULT 5
 HV3K_HUMAN STANDARD; PRT; 126 AA.
 AC P01772.1
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION KOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_TaxID:9606;
 RP SEQUENCE. AND DISULFIDE BONDS.
 RA MEDLINE:8328933; PubMed:6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hiltmann N.;
 RT Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.
 RL J. Mol. Biol. 209:391-391(1980).
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE:81072295; PubMed:7441755.
 RA Marguier M., Deisenhofer J., Huber R., Palm W.;
 RT Crystallographic refinement and atomic models of the intact
 RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 resolution.
 DR J. Mol. Biol. 209:391-391(1980).
 DR PIR: A02055; Q1HUB1.
 DR PDB: 2PB4; 12-JUL-89.
 DR InterPro: IPR003006.
 DR Pfam: PF00047.19.1.
 KW Immunoglobulin V region: 3D-structure.
 RM MOD_RES 122 96
 FT MOD_RES 122 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT HELIX 29 31

PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT STRAND 105 110
 FT STRAND 3 7
 FT TURN 14 15
 FT STRAND 18 25
 FT HELIX 29 31


```

DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
OS Carassius auratus (Goldfish).
NC Actinopterygii: Cyprinidae: Cyprininae: Carassius.
CC NCBI_TaxID=7957;
RN [1]
RP MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Watt G.M.;
RT "Immunoglobulin heavy chain gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
CC -----
CC This SMS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use. The EMBL outstation at the European Bioinformatics Institute has
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J03616; AAA50807.1;
DR FRS: A28966; A28966;
DR InterPro: IPR003006;
DR Pfam: PF00047; 19; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 20 50 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 20 51 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 512652503FA6E6B CRC64;

Query Match 51.78; Score 46; DB 1; Length 117;
Best Local Similarity 56.28; Pred. No. 0.44;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IKQDSERYKADSVG 17
DB 70 IYDQSDVYADTVKG 85
1 |||: |||:|:|
1 |||: |||:|:|

RESULT 13
REV3_HUMAN STANDARD: PRT; 121 AA.
ID HV53_HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION H1L.
OS Homo sapiens (Human).
NC Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
CC NCBI_TaxID=9606;
RN [1]
RP MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.R., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RT cytomunoglobulin IgG H1L."
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGSI MYELOMA
CC CELL.
CC PROTEIN.
CC PIR: A04549;
CC HSP: P01772; Q1G3.
```

```

DR InterPro: IPR003006;
DR EMBL: F00047; 19; 1.
DR FRS: A28966; A28966;
DR Non_TER 121 121
SQ SEQUENCE 121 AA; 480FC53610EFD5DAB CRC64;

Query Match 51.78; Score 46; DB 1; Length 121;
Best Local Similarity 61.58; Pred. No. 0.46;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 DQSEKRYADSVG 17
DB 54 NQSMRYGDVSG 66
-|| || |||:|
-|| || |||:|

RESULT 14
REV7_MOUSE STANDARD: PRT; 98 AA.
ID HV57_MOUSE
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 6.96.
NC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BA1B/CJ.19; PubMed=2199654;
RA MEDLINE=69719113; Lopez de Castro J.R., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR InterPro: IPR003006;
DR Pfam: PF00047; 19; 1.
KM Immunoglobulin V region.
KM Non_TER 98 98
SQ SEQUENCE 98 AA; B8644F792PEB5B CRC64;

Query Match 50.68; Score 45; DB 1; Length 98;
Best Local Similarity 56.28; Pred. No. 0.54;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 IKQDSERYKADSVG 17
DB 51 ISDQSDVYPPDSVG 66
1 || || |||:|
1 || || |||:|

RESULT 15
REV5_CARRAU STANDARD: PRT; 116 AA.
ID HV05_CARRAU
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
NC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi:
CC Cypriniformes: Cyprinidae: Cyprininae: Carassius.
CC NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Watt G.M.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
```

RT and family relationships of two genes and a pseudogene in a telocent
 RT Fish.
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 RL RT: B88966; B88966.
 DR Locus: 188000000.
 DR Pfam: PF00047; 197.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT CHAIN 19
 FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 20 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 20 34 FRAMEWORK 2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 85 116 FRAMEWORK 3.
 FT DISULFID 41 114 BY SIMILARITY.
 FT NON_TER 116
 SQ SEQUENCE 116 AA: 12808 MW: 922279ZDPF199B12 CRC64:

Query Match 50.64; Score 45; DB 1; Length 116;
 Best Local Similarity 66.78; Pred. No. 0.65;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 GSEXYADSYRG 17
 1 |||||:|
 DB 73 GSEXYADSYRG 84

Search completed: November 19, 2001, 08:25:34
 Job time: 722 sec

Best Local Similarity 75.0%; Pred. No. 0.0025;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 IKDGSERYADSVG 17
1 ||| ||||| |||

DB 51 ISYDGSNRYADSVG 66

RESULT 6 PRELIMINARY: PRT: 77 AA.

ID 09UL76
AC 09UL76
DT 01-MAY-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fischer M., Kueppers R.;
RC TISSUE-INTEREST:
RT Human IgH and Igk secreting intestinal plasma cells carry heavily
mutated heavy chain genes, the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AJ009523; CAA08730.1; -.
DR InterPro: IPR003006; -.
DR SwissProt; P00047; I9.1.1.
DR SRA; PF00047; I9.1.1.
FT NON_TER 77 77
FT 100TER 100 100
SQ SEQUENCE 77 AA: 9022 MW: ADA20FE45E13D9A8 CRC64;

Query Match 71.9%; Score 64; DB 4; Length 77;
Best Local Similarity 68.8%; Pred. No. 0.0034; 3; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 IKDGSERYADSVG 17
1 ||| ||||| |||

DB 20 INEDGSERYADSVG 35

RESULT 7 PRELIMINARY: PRT: 116 AA.

ID 09UL93
AC 09UL93
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE AUTOANTIBODIES IN RHEUMATIC CARDITIS AND NORMAL
FELUS D.C.;
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Young D.C., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT Myosin-reactive autoantibodies in rheumatic carditis and normal
felus.;
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AF015021; AAD56257.1; -.
DR InterPro: IPR003006; -.

DR InterPro: IPR003596; -.
DR Pfam: PF00047; I9.1.
DR SRA; PF00047; I9.1.
FT NON_TER 116 116
FT 100TER 100 100
SQ SEQUENCE 116 AA: 12434 MW: 0DA0348154DD6061 CRC64;

Query Match 71.9%; Score 64; DB 4; Length 116;

Best Local Similarity 75.0%; Pred. No. 0.0034; 3; Indels 0; Gaps 0;

OY 2 IKDGSERYADSVG 17
1 ||| ||||| |||

DB 50 ISYDGSNRYADSVG 65

RESULT 8 PRELIMINARY: PRT: 122 AA.

ID 09UL84
AC 09UL84
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-9827139; PubMed-9614934;
RT Young D.C., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
felus";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AF015021; AAD56256.1; -.
DR SRA; PF01772; 2PRL
DR InterPro: IPR003006; -.
DR Pfam: PF00047; I9.1.1.
DR SMART; SM00406; I9.1.1.
FT NON_TER 122 122
FT 100TER 100 100
SQ SEQUENCE 122 AA: 13579 MW: 3605404136543B8 CRC64;

Query Match 68.5%; Score 61; DB 4; Length 122;

Best Local Similarity 68.8%; Pred. No. 0.018; 3; Indels 0; Gaps 0;

OY 2 IKDGSERYADSVG 17
1 ||| ||||| |||

DB 51 ISNDSNRYADSVG 66

RESULT 9 PRELIMINARY: PRT: 121 AA.

ID 09UL71
AC 09UL71
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.


```

RESULT 13
09UL72 ID 09UL72 PRELIMINARY; PRT: 118 AA.
AC 09UL72:
DT 01-MAY-2000 (TRFMBLrel. 13, Created)
DT 01-MAY-2000 (TRFMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRFMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Caniellota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN NCBI_TaxID=9606;
RX NUCLEOTIDE SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998);
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DR EMBL: AF035042; AAD56278.1;
DR HSPB: P01772; 2F84.
DR InterPro: IPR003006;
DR InterPro: IPR003596;
DR Pfam: PF00047; 19; 1.
DR SMART: SM00406; 19; 1.
DR NCBI: 118
DR NCBI: 118
PT NON-TER
SQ SEQUENCE 118 AA; 12872 MW; B401A594B2D5CCA CRC64;

Query Match 53.9%; Score 48; DB 4; Length 118;
Best Local Similarity 47.1%; Pred. No. 2.2;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 1 NIKODSEKRYADSVK 17
Db 49 SVYSGSSRYADSVK 65

RESULT 14
09CV6 ID 09CV6 PRELIMINARY; PRT: 594 AA.
AC 09CV6:
DT 01-MAY-1999 (TRFMBLrel. 10, Created)
DT 01-MAY-1999 (TRFMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TRFMBLrel. 13, Last annotation update)
DE PENTICILIN-BINDING PROTEIN (PBPA1).
OS R. solis.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN NCBI_TaxID=782;
RX NUCLEOTIDE SEQUENCE FROM N.A.
RX STRAIN=MDRI2.E.
RX PubMed=9823993;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Scharitz-Ponten T., Almark U.C.M., Podowski R.M., Neeblund A.K.,
RA Eriksson A.-S., Winkler H.H., Kuriland C.G.;
RA "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria";
RL Nature 368:133-140(1998);
RX EMBL: AF013401.1;
RX PubMed=9801460;
DR Pfam: PF00095; Transmembrane; 1.
SQ SEQUENCE 594 AA; 67195 MW; 669AB06AD428AC CRC64;

```

Query Match 53.9%; Score 48; DB 2; Length 594;
 Best Local Similarity 52.9%; Pred. No. 14;

```

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 NIKODSEKRYADSVK 17
Db 194 NIKODSEKRYADSVK 210

RESULT 15
09VZ9 ID 09VZ9 PRELIMINARY; PRT: 235 AA.
AC 09VZ9:
DT 01-MAY-2000 (TRFMBLrel. 13, Created)
DT 01-MAY-2000 (TRFMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRFMBLrel. 14, Last annotation update)
DE CG1259 PROTEIN.
GN CG1259.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Psocodea; Neoptera; Psocoptera; Psocidae; Blattellidae; Muscomorpha;
OC Diptera; Diptera; Phlebotomidae; Diptophila.
RN NCBI_TaxID=7227;
RX NUCLEOTIDE SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Gunkler S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Gunkler S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Gage R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt J., Andrews-Pfannkoch K.,
RA Bell R.M., Bass A., Baxendale J., Baxendale J., Baxendale J.,
RA Beecher D., Bockemuehl M.R., Brock J., Brockstein P., Brodt P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA DePamphilis M., Delcher A., Deng Z., Davis A.D., Dew T., Dietz S.M.,
RA Dodson K., Dou P.L.E., Doves M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrar G., Gabor C., Gabor C.,
RA Gabor C., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegyan C.,
RA Jatalin B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B., Kodali C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Malet B., McIntosh T.C., McLeod G., Meng L., Meng L.,
RA Merklow G., Mervin Murphy B., Murphy L., Murphy L., Murphy L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussbaum D.R., Pacleb J.M.,
RA Palazolo M., Plittman G.S., Pan S., Pollard J., Puri V., Reese H.G.,
RA Reinert K., Remington K., Sanders R.D.C., Schneider F., Shen H.,
RA Shie B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Teeter C., Turner M., Winkler G.M., Winkler G.M.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye T., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X.,
RA Zhong X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000);
RX EMBL: F00005513;
DR InterPro: IPR000513; CG1259.
DR Pfam: PF000379; insect_cuticle; 1.
DR PRINTS: PS00947; CUTICLE.
DR PROSITE: PS00233; CUTICLE.
SQ SEQUENCE 235 AA; 23066 MW; A9DC2E7914B5A68 CRC64;

```

Query Match 53.4%; Score 47.5; DB 5; Length 235;

Best Local Similarity 52.6%; Pred. NO. 5.7;
Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 1;
OY 2 IKQGSFK---YYADSVRG 17
I: III: IIIII:
Db 167 IEPDGSRIYVYYADSDING 185

Search completed: November 19, 2001, 08:25:01
Job time: 739 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:12:34 ; Search time 77.92 Seconds

(without alignments)
13,226 Million cell updates/sec

Title: US-09-610-118-62

Sequence: 1 NIKOGSEKRYADSVRG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :
1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDSB/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDSB/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDSB/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDSB/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDSB/gcgdata/geneseq/geneseqp/AA1997.DAT:*
18: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
19: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
20: /SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDSB/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDSB/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	36	AA852064	Heavy chain variab
2	82	92.1	98	AA872074	DP24 VH region. H
3	82	92.1	98	AA840138	Anti-hIL12 antiod
4	82	92.1	98	AA840140	Anti-hIL12 antiod
5	82	92.1	117	AA863601	Human immunoglob
6	82	92.1	125	AA862766	Human HIV-1 monoc
7	82	92.1	211	AA853122	Single chain Apo-2
8	82	92.1	17	AA850449	Tumour antigen ant
9	82	92.1	17	AA850449	Tumour antigen ant
10	82	92.1	17	AA850449	Tumour antigen ant
11	82	92.1	17	AA850449	Tumour antigen ant
12	82	92.1	17	AA850449	Tumour antigen ant
13	82	92.1	17	AA850449	Tumour antigen ant
14	82	92.1	17	AA850449	Tumour antigen ant
15	82	92.1	17	AA850449	Tumour antigen ant
16	82	92.1	17	AA850449	Tumour antigen ant
17	82	92.1	17	AA850449	Tumour antigen ant
18	82	92.1	17	AA850449	Tumour antigen ant
19	82	92.1	17	AA850449	Tumour antigen ant
20	82	92.1	17	AA850449	Tumour antigen ant
21	82	92.1	17	AA850449	Tumour antigen ant
22	82	92.1	17	AA850449	Tumour antigen ant
23	82	92.1	17	AA850449	Tumour antigen ant
24	82	92.1	17	AA850449	Tumour antigen ant
25	82	92.1	17	AA850449	Tumour antigen ant
26	82	92.1	17	AA850449	Tumour antigen ant
27	82	92.1	17	AA850449	Tumour antigen ant
28	82	92.1	17	AA850449	Tumour antigen ant
29	82	92.1	17	AA850449	Tumour antigen ant
30	82	92.1	17	AA850449	Tumour antigen ant
31	82	92.1	17	AA850449	Tumour antigen ant
32	82	92.1	17	AA850449	Tumour antigen ant
33	82	92.1	17	AA850449	Tumour antigen ant
34	82	92.1	17	AA850449	Tumour antigen ant
35	82	92.1	17	AA850449	Tumour antigen ant
36	82	92.1	17	AA850449	Tumour antigen ant
37	82	92.1	17	AA850449	Tumour antigen ant
38	82	92.1	17	AA850449	Tumour antigen ant
39	82	92.1	17	AA850449	Tumour antigen ant
40	82	92.1	17	AA850449	Tumour antigen ant
41	82	92.1	17	AA850449	Tumour antigen ant
42	82	92.1	17	AA850449	Tumour antigen ant
43	82	92.1	17	AA850449	Tumour antigen ant
44	82	92.1	17	AA850449	Tumour antigen ant
45	82	92.1	17	AA850449	Tumour antigen ant

12	72	80.9	17	AA83984	Anti-hIL12 antiod
13	71	79.8	130	AA824537	Immunoglobulin F10
14	69	77.5	17	AA839833	Anti-hIL12 antiod
15	69	77.5	116	AA866340	Human immunoglob
16	67	75.3	17	AA839822	Anti-hIL12 antiod
17	67	75.3	123	AA862778	Human HIV-1 monoc
18	67	75.3	17	AA839847	Anti-hIL12 antiod
19	66	74.2	17	AA839833	Anti-hIL12 antiod
20	66	74.2	17	AA839822	Anti-hIL12 antiod
21	66	74.2	17	AA839840	Anti-hIL12 antiod
22	66	74.2	17	AA839833	Anti-hIL12 antiod
23	66	74.2	17	AA839822	Anti-hIL12 antiod
24	66	74.2	17	AA839847	Anti-hIL12 antiod
25	66	74.2	17	AA839833	Anti-hIL12 antiod
26	66	74.2	17	AA839822	Anti-hIL12 antiod
27	66	74.2	17	AA839840	Anti-hIL12 antiod
28	66	74.2	17	AA839833	Anti-hIL12 antiod
29	66	74.2	17	AA839822	Anti-hIL12 antiod
30	66	74.2	17	AA839847	Anti-hIL12 antiod
31	66	74.2	17	AA839833	Anti-hIL12 antiod
32	66	74.2	17	AA839822	Anti-hIL12 antiod
33	66	74.2	17	AA839840	Anti-hIL12 antiod
34	66	74.2	17	AA839833	Anti-hIL12 antiod
35	66	74.2	17	AA839822	Anti-hIL12 antiod
36	66	74.2	17	AA839840	Anti-hIL12 antiod
37	66	74.2	17	AA839833	Anti-hIL12 antiod
38	66	74.2	17	AA839822	Anti-hIL12 antiod
39	66	74.2	17	AA839840	Anti-hIL12 antiod
40	66	74.2	17	AA839833	Anti-hIL12 antiod
41	66	74.2	17	AA839822	Anti-hIL12 antiod
42	66	74.2	17	AA839840	Anti-hIL12 antiod
43	66	74.2	17	AA839833	Anti-hIL12 antiod
44	66	74.2	17	AA839822	Anti-hIL12 antiod
45	66	74.2	17	AA839840	Anti-hIL12 antiod

ALIGNMENTS

RESULT 1	AA861294	standard: Peptide; 17 AA.
ID	AA861294	
AC	AA861294	
XX	04-APR-2001	(first entry)
XX	Anti-TNCO 268 scFv CDR, SEQ ID NO: 62.	
XX	Human: antibody; scFv; CDR: complementarily determining region;	
XX	TNCO 268; carianti; cerebroprotective; cytostatic; antitumor;	
XX	thrombolytic; antiarteriosclerotic; hemostatic; glycoprotein VI; Gvvi;	
XX	platelet membrane glycoprotein receptor; bleeding disorder;	
XX	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;	
XX	ischemia; cardiovascular disease; immunological disease; liver disorder;	
XX	cancer.	
XX	Homo sapiens.	
XX	MO20010810-A1.	
XX	04-JAN-2001.	
XX	30-JUN-2000; 2000MO-US18152.	
XX	30-JUN-1999; 99US-0343468.	
XX	06-DEC-1999; 99US-0454824.	
XX	14-FEB-2000; 2000US-0503877.	
XX	(MIL-1) MILLENNIUM PHARM INC.	
XX	Buefield SJ, Villalobos J, Jandrot-Perrus M, Valinchenko W, Gill DS,	
XX	Qian MD, Kingsbury G;	

XX WPI: 2001-080877/09.
 XX New genes encoding human platelet-expressed collagen receptor,
 XX glycoprotein VI (GPVI), also called platelet membrane glycoprotein receptor
 XX and diagnosing hemorrhagic disorders, thrombotic diseases and
 XX immunological disorders -
 XX
 XX Claim 31: Page 102: 227pp: English.
 XX
 XX The present sequence is given in a specification relating to an isolated
 XX nucleic acid sequence encoding a platelet membrane glycoprotein receptor
 XX glycoprotein VI (GPVI), also called platelet membrane glycoprotein receptor
 XX and polypeptides and their modulators e.g. antisense oligonucleotides,
 XX ribozymes and antibodies, are useful for preventing, treating and
 XX diagnosing disorders associated with aberrant expression or activity of
 XX GPVI. These disorders include bleeding disorders
 XX (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
 XX (e.g. thrombosis), hypertension, the coronary arteries, haemorrhagic
 XX disorders, coronary artery and blood vessel diseases (e.g. stroke and
 XX ischaemia), cardiovascular diseases (e.g. atherosclerosis), placental
 XX infarction), immunological diseases (e.g. platelet disorder) and
 XX embryonic liver disorders. Preferably they are used to prevent acute
 XX cardiac ischaemia following angioplasty and metastatic cancers,
 XX especially of the colon and liver.
 XX
 XX Sequence 17 AA:
 SO
 Query Match 100.0%; Score 89; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1,1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIKQDSKKRYADSVG 17
 ||||||||||||||||
 Db 1 nlkqgsekyyadvsg 17
 RESULT 2
 AAR52066 standard; Protein: 98 AA.
 XX
 XX AAR52066:
 XX
 XX 11-OCT-1996 (first entry)
 XX
 XX Heavy chain variable region of human PLO123 antibody.
 XX
 XX antibody: humanised; murine: human; heavy chain; light variable;
 XX framework region; complementarity determining region; reshaping;
 XX modelling; surface residue; modify.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Region 1..30
 XX /label= "FR 1"
 XX /note= "framework_region_1"
 XX Region 31..35
 XX /label= "CDR 1"
 XX /note= "complementarity-determining_region_1"
 XX Region 36..45
 XX /label= "CDR 2"
 XX /note= "FR 2"
 XX Region 50..59
 XX /note= "CDR 2"
 XX Region 60..98
 XX /note= "FR 3"
 XX
 XX BPS92106-A1.
 XX 13-APR-1994.
 XX PD
 XX 07-SEP-1993; 93EP-0307051.

XX 09-SEP-1992; 92US-0942245.
 XX (PEDER/ PEDERSEN J T.
 XX (IMMUN-) IMMUNOCEN INC.
 XX
 XX Guild BC, Pedersen JT, Rees AR, Roguska MN, Searle SMJ:
 XX WPI: 1994-120230/15.
 XX
 XX Method of resurfacing of rodent antibodies to produce humanised
 XX antibody forms - for producing non-human antibodies with improved
 XX therapeutic efficiency by presenting human surface on V-region
 XX
 XX Example 1: Fig 4b: 230pp: English.
 XX
 XX Modification of a rodent antibody (Ab) or fragment by resurfacing in
 XX order to produce a humanised rodent Ab can be determined by calculating
 XX the homology between murine and human Ab antibody surfaces. In order to test
 XX the resurfacing approach of the invention, three humanisation
 XX experiments were set up: (1) traditional loop grafting; (2) resurfacing
 XX using most similar chain; and (3) resurfacing approach using
 XX human sequence. The results are shown in Table 1. The Ab used was the
 XX murine anti-N901 Ab (see AAR52061). Experimental results show that
 XX the present sequence which represents the human PLO123 Ab light chain
 XX (AAR52057) was prepd. by resurfacing. Sequence numbering starts at
 XX position 118 in the specification.
 XX
 XX Sequence 98 AA:
 SO
 Query Match 92.1%; Score 82; DB 15; Length 98;
 Best Local Similarity 88.2%; Pred. No. 1,2e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NIKQDSKKRYADSVG 17
 ||||||||||||||||
 Db 50 nlkqgsekyyadvsg 66
 RESULT 3
 AAR72074 standard; Protein: 98 AA.
 XX
 XX AAR72074:
 XX
 XX 26-SEP-1995 (first entry)
 XX
 XX DP54 VH region.
 XX
 XX Graves ophthalmopathy associated immunoglobulin protein;
 XX orbital antigen; monoclonal antibody; heavy chain; H chain;
 XX variable region; autoimmunity.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Region 41..44
 XX /label= "CDR1"
 XX /note= "CDR1"
 XX Region 49..67
 XX /label= "CDR2"
 XX W09508336-A.
 XX 30-MAR-1995.
 XX PD
 XX 22-SEP-1994; 94MO-US10756.
 XX 22-SEP-1993; 93US-0124469.
 XX (NICH-) NICHOLS INST DIAGNOSTICS.

PI Molachlan SM, Rapoport B.
 DR WPI: 1995-139353/19.
 DR N-PSDB: AA089332.
 XX
 XX Graves' ophthalmopathy-associated monoclonal antibody - produced
 XX by molecular cloning of immunoglobulin genes by PCR
 XX
 XX Disclosure: Page 72: 94pp: English.
 XX
 XX L- and H-chain DNA was amplified by PCR from Graves' orbital
 XX tissue and clones encoding autoimmune-associated immunoglobulin
 XX fragments were obtained. 2/15 clones of H chain IgG1 genes codes
 XX for a protein of 350 amino acids. The complete H chain cDNA encodes
 XX a protein of 350 amino acids. The complete L chain cDNA encodes
 XX a protein of 275 amino acids. The DNA (AA089333) and corresp. amino
 XX acid (AA0872075) sequences of the VH region of a representative clone,
 XX 057H1.19, are provided.
 XX
 XX Sequence 98 AA:
 XX
 XX Query Match 92.1%; Score 82; DB 16; Length 98;
 XX Best Local Similarity 89.2%; Pred. No. 1.2e-06;
 XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0
 XX
 XX Qy 1 NIKDGGSEKRYVDSVNG 17
 XX |||||
 XX Db 50 ALKADSEKYYDSVNG 66
 XX
 XX RESULT 4
 XX ABA40138
 XX ID ABA40138 standard: Protein: 98 AA.
 XX AC ABA40138:
 XX AD 05-FEB-2001 (first entry)
 XX DE Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 664.
 XX
 XX Human: neutralising antibody: Interleukin-12; IL-12; antiInflammatoxy;
 XX complementarily determining region; CDR; antiPneumatic; antiarthritic;
 XX antileptoretic; neuroprotective; antiproliferative; antiaesthetic; cardiac;
 XX antiparasitic; antidiabetic; immunosuppressive; Crohn's disease;
 XX multiple sclerosis; rheumatoid arthritis.
 XX
 XX Homo sapiens.
 XX
 XX MO20005672-A1.
 XX
 XX PD 28-SEP-2000.
 XX
 XX PD 24-MAR-2000: 2000MO-US07946.
 XX
 XX XR 25-MAR-1999: 99US-0126603.
 XX
 XX (BADI) BASF AG.
 XX (GENY) GENENTEC INST INC.
 XX
 XX Seinfeld JG, Roguska M, Parkin M, Buerjee S, Tracey DE, White M;
 XX Sullivan J, Sussman M, Berman NM, Erickson S, Wykes A,
 XX Pridmore G, Venturini A, Weldon M, Elvin JG, Duncan AR;
 XX Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
 XX WPI: 2000-638250/61.
 XX
 XX New human antibody specific for human Interleukin-12 (IL-12) used to
 XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 XX disease and multiple sclerosis -
 XX
 XX Claim 75: Page 122: 377pp: English.
 XX
 XX This invention relates to a new human antibody specific for human

[illegible]

```
Query Match          92.18; Score 62; DB 21; Length 96;
Best local similarity 88.24; Prod. No. 1.2e-06;
Matches    15; Conservative   1; Mismatches    1; Indels      0; Gaps      0;
```

heavy chain sequences (AAR6525-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAR78939-79002) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M31, by PCR

Query Match	92.1%	Score 82	DB 16	Length 117
Best Local Similarity	88.2%	Pred. No. 1.5e-06		
Matches	15	Conservative	1	Mismatches 1; Indels 0; Gaps 0
Q7	1	NTKDGSEKYYADSVG	17	
Db	69	nltkdgsekyadvsg	85	

DT	03-APR-2001	(first entry)
XX		
DE	Human HIV-1 monoclonal antibody SEQ ID NO: 75.	
XX		
XX		
KM	Human immunodeficiency virus-1; HIV-1; human monoclonal antibody-envelope glycoprotein, gp120; diagnosis.	
KM		
XX		

Query Match	92.1%	Score 82	DB 22	length 125
Best Local Similarity	88.2%	Pred. No. 1.7e-06		
Matches 15	Conservative 1	Mismatches 1	Indels 0	Gaps 0
1 NIKODSGERYADSVNG 17				

```

DB      51 ntkdgssekyydvsvkg 67
      |||||
RESULT  8
ID      AAM90180
AC      AAM90180 standard; Protein: 271 AA.
XX
XX      AAM90180:
XX
XX      10-MAY-1999 (first entry)
XX
XX      Human clone A6 fusion protein antibody.
XX
XX      Antibody: human; clone A6; hAb; fusion protein; polyclonal tag;
XX      Western blot; enzyme-linked immunosorbent assay; ELISA; therapy;
XX      immunofluorescence; immunoprecipitation assay; affinity purification;
XX      diagnosis; vaccine; serum; immune response.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Protein  1..271
XX      /note="Partial coding sequence, no stop codon given"
XX
XX      WC0901475-A2.
XX
XX      14-JAN-1999.
XX
XX      03-JUL-1998: 98MO-DE01882.
XX
XX      04-JUL-1997: 97DE-1028697.
XX
XX      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX      Braunagel M, Doerflam H, Kiprianov S, Kuerschner T;
XX      Little M, Welschof M;
XX      WPI: 1999-106000/09.
XX      N-PSDB: AAV74274.
XX
XX      Human antibody against fusion protein with polyclonal tag -
XX      derived as standard in the process of purification,
XX      diagnosis and therapy and for preparing vaccines
XX
XX      Claim 4: 20pp. German.
XX
XX      This invention describes a human antibody (hAb) against a fusion
XX      (poly)peptide or protein that includes a segment of at least 6
XX      consecutive amino acid residues. This antibody is useful in
XX      immunodiagnosis, immunotherapy, immunoprecipitation, immunofluorescence or
XX      immunoprecipitation assays. Also hAb can be used for affinity
XX      purification of the protein, for in vivo diagnosis or therapy, and
XX      in production of vaccines. hAb are universally applicable
XX      alternatives to human serum. They are specific for the polyclonal
XX      tag, regardless of the nature of the rest of the protein. Since hAb
XX      are not produced in an animal, they contain no components that can
XX      induce an immune response in humans.
XX
XX      Sequence 271 AA:
XX
Query Match      92.18; Score 82; DB 20; Length 271;
Best Local Similarity 88.28; Pred No. 46-06; 1: Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches
OY      1 NTKDGSSEKYYDVSVKG 17
      |||||
DB      52 ntkdgssekyydvsvkg 68

```

```

ID      AAM83323 standard; Protein: 312 AA.
XX
XX      AAM83323:
XX
XX      16-MAR-1999 (first entry)
XX
XX      Single chain Apo-2 antibody 2066.
XX
XX      Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
XX      tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
XX      TNF cytokine.
XX
XX      Homo sapiens.
XX
XX      WC09851793-A1.
XX
XX      19-NOV-1998.
XX
XX      14-MAY-1998: 98MO-US09704.
XX
XX      09-FEB-1998: 98US-0020746.
XX
XX      15-MAY-1997: 97US-0857216.
XX
XX      (GETH) GENENTECH INC.
XX
XX      Adams CM, Ashkenazi AJ, Chuntarapatt A, Kim KJ;
XX      WPI: 1999-045228/04.
XX      N-PSDB: AAV72533.
XX
XX      Human Apo-2 polypeptide inducing apoptosis - useful to treat
XX      conditions linked with decreased apoptosis e.g. cancer, and produce
XX      antibodies to increase or decrease apoptosis
XX
XX      Example 14: Fig 16; 134pp; English.
XX
XX      The present invention describes human Apo-2. Apo-2 can be used
XX      therapeutically to induce apoptosis in mammalian cells, and so is useful
XX      to treat conditions associated with decreased apoptosis e.g. cancer.
XX      Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor by
XX      (TNFR). TNF cytokines can trigger caspase-dependent apoptosis. It
XX      can be used to identify agents activating Apo-2, useful to treat
XX      mammalian cancer cells, and to produce Apo-2 chimera useful
XX      therapeutically (e.g. those containing immunoglobulin sequences can be
XX      inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
XX      tag polypeptide allow Apo-2 detection and purification using anti-tag
XX      antibodies). It can be used to produce antibodies against Apo-2 and
XX      utilized (part produce) as a carrier in compositions
XX      comprising first and second Apo-2 antibodies). Agonistic (especially
XX      single-chain) antibodies can be administered to induce apoptosis in
XX      mammalian cancer cells, and antagonistic antibodies used to block
XX      excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
XX      antibodies may also be used diagnostically e.g. to detect
XX      expression in cells/tissues.
XX      sequence representative of a single chain Apo-2 antibody, designated 2066.
XX
XX      Sequence 312 AA:
XX
Query Match      92.18; Score 82; DB 20; Length 312;
Best Local Similarity 88.28; Pred No. 46-06; 1: Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches
OY      1 NTKDGSSEKYYDVSVKG 17
      |||||
DB      89 ntkdgssekyydvsvkg 105

```

```

RESULT  10
ID      AAY05049
      AAY05049 standard; peptide: 17 AA.

```

[illegible]

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OW protein - protein search, using sw model

Run on: November 19, 2001, 08:23:14 ; Search time 526.89 Seconds
(without alignments)

8.959 Million cell updates/sec

Title: US-09-610-118-62

Perfect score: 89

Sequence: 1 NIKODSEKRYADSVRG 17

Scoring table:

BLOSUM62

Gapex 10.0, Gapext 0.5

Searched:

3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters:

3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Pending Patents.AL.Maln.*
1: /cgn2_6/pdata/2/paa/PCUTUS.COMB.pep.*
2: /cgn2_6/pdata/2/paa/US06.COMB.pep.*
3: /cgn2_6/pdata/2/paa/US07.COMB.pep.*
4: /cgn2_6/pdata/2/paa/US08.COMB.pep.*
5: /cgn2_6/pdata/2/paa/US082.COMB.pep.*
6: /cgn2_6/pdata/2/paa/US082.COMB.pep.*
7: /cgn2_6/pdata/2/paa/US084.COMB.pep.*
8: /cgn2_6/pdata/2/paa/US084.COMB.pep.*
9: /cgn2_6/pdata/2/paa/US085.COMB.pep.*
10: /cgn2_6/pdata/2/paa/US085.COMB.pep.*
11: /cgn2_6/pdata/2/paa/US085.COMB.pep.*
12: /cgn2_6/pdata/2/paa/US085.COMB.pep.*
13: /cgn2_6/pdata/2/paa/US085.COMB.pep.*
14: /cgn2_6/pdata/2/paa/US085.COMB.pep.*
15: /cgn2_6/pdata/2/paa/US091.COMB.pep.*
16: /cgn2_6/pdata/2/paa/US092.COMB.pep.*
17: /cgn2_6/pdata/2/paa/US093.COMB.pep.*
18: /cgn2_6/pdata/2/paa/US094.COMB.pep.*
19: /cgn2_6/pdata/2/paa/US094.COMB.pep.*
20: /cgn2_6/pdata/2/paa/US094.COMB.pep.*
21: /cgn2_6/pdata/2/paa/US094.COMB.pep.*
22: /cgn2_6/pdata/2/paa/US094.COMB.pep.*
23: /cgn2_6/pdata/2/paa/US094.COMB.pep.*
24: /cgn2_6/pdata/2/paa/US094.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the target being printed, and is derived by analysis of the local score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100	17	PCT-US00-18152-62	Sequence 62, App1
2	89	100	17	US-09-610-118-62	Sequence 62, App1
3	89	100	17	US-09-610-118-62	Sequence 62, App1
4	82	92.1	98	PCT-US00-07946-664	Sequence 666, App
5	82	92.1	98	PCT-US00-07946-666	Sequence 666, App
6	82	92.1	98	US-08-124-469-32	Sequence 32, App1
7	82	92.1	98	US-08-412-771-32	Sequence 32, App1
8	82	92.1	98	US-08-456-207-64	Sequence 32, App1
9	82	92.1	98	US-09-534-717-664	Sequence 664, App1

10	82	92.1	98	US-09-534-717-666	Sequence 666, App1
11	82	92.1	98	US-09-755-181-65	Sequence 65, App1
12	82	92.1	124	US-60-141-701-75	Sequence 75, App1
13	82	92.1	134	US-09-811-737-3	Sequence 3, App1
14	82	92.1	241	PCT-US01-1910-1889	Sequence 1889, App
15	82	92.1	241	US-09-880-748-1470	Sequence 1470, App
16	82	92.1	247	PCT-US01-1910-1470	Sequence 1470, App
17	82	92.1	247	US-09-880-748-1470	Sequence 1470, App
18	82	92.1	251	PCT-US00-07946-664	Sequence 666, App
19	82	92.1	251	US-08-456-207-64	Sequence 32, App1
20	82	92.1	253	PCT-US01-1910-1003	Sequence 1003, App
21	82	92.1	253	PCT-US01-1910-1003	Sequence 1003, App
22	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
23	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
24	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
25	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
26	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
27	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
28	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
29	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
30	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
31	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
32	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
33	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
34	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
35	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
36	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
37	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
38	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
39	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
40	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
41	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
42	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
43	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
44	82	92.1	253	US-09-880-748-1003	Sequence 1003, App
45	82	92.1	253	US-09-880-748-1003	Sequence 1003, App

ALIGNMENTS

RESULT 1
PCT-US00-18152-62
Sequence 62, Application PC/US0018152
GENERAL INFORMATION:
TITLE OF INVENTION: GYPCOPROTEIN VI AND USGS THEREOF
FILE REFERENCE: 7853-211-228 PCT/US00/018152
CURRENT APPLICATION NUMBER: 09/503,387
EARLIER FILING DATE: 2/14/00
EARLIER APPLICATION NUMBER: 09/503,387
EARLIER FILING DATE: 12/6/99
EARLIER APPLICATION NUMBER: 09/345,468
EARLIER FILING DATE: 6/20/99
NUMBER OF SEQ NOS: 72
SEQUENCE IDENTIFIED FOR WINDOWS Version 3.0
SEQ ID NO 62
LENGTH: 17
TYPE: PPT
ORGANISM: Homo sapiens
PCT-US00-18152-62

Query Match 100.0%; Score 89; DB 1; Length 17;
Best local similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 NIKODSEKRYADSVRG 17
1 NIKODSEKRYADSVRG 17

```

RESULT 2
US-09-610-118-62
; Sequence 62, Application US/09610118
; GENERAL INFORMATION:
; APPLICANT: Bufield, S.
; APPLICANT: Villavall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; APPLICANT: Gili, D.
; APPLICANT: Klingbein, G.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-211
; CURRENT FILING DATE: US/09/610, 118
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 12/6/99
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 6/30/99
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-610-118-62

```

```

Query Match
Best Local Similarity 100.0%; Score 89; DB 20; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NIKOGSEKRYADSVNG 17
DB 1 NIKOGSEKRYADSVNG 17

```

```

RESULT 3
US-09-832-312-62
; Sequence 62, Application US/09832312
; GENERAL INFORMATION:
; APPLICANT: Bufield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT FILING DATE: US/09/832, 312
; PRIOR APPLICATION NUMBER: 09/610, 118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503, 387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454, 824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/445, 468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-62

```

```

Query Match
Best Local Similarity 100.0%; Score 89; DB 22; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIKOGSEKRYADSVNG 17
DB 1 NIKOGSEKRYADSVNG 17

```

```

RESULT 4
PCT-US00-07946-664
; Sequence 664, Application PC/TUS0007946
; GENERAL INFORMATION:
; APPLICANT: Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Product
; FILE REFERENCE: BBI-093CPC
; CURRENT FILING DATE: PCT/US00/07946
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: MATCH 25, 1999
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: MATCH 25, 1999
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-07946-664

```

```

Query Match
Best Local Similarity 92.1%; Score 82; DB 1; Length 98;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NIKOGSEKRYADSVNG 17
DB 50 NIKOGSEKRYADSVNG 66

```

```

RESULT 5
PCT-US00-07946-666
; Sequence 666, Application PC/TUS0007946
; GENERAL INFORMATION:
; APPLICANT: Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Product
; FILE REFERENCE: BBI-093CPC
; CURRENT FILING DATE: PCT/US00/07946
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: MATCH 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 666
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-07946-666

```

```

Query Match
Best Local Similarity 92.1%; Score 82; DB 1; Length 98;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NIKOGSEKRYADSVNG 17
DB 50 NIKOGSEKRYADSVNG 66

```

```

RESULT 6
US-08-124-469-32
; Sequence 32, Application US/08124469
; GENERAL INFORMATION:
; APPLICANT: KAPORONT, Basil
; APPLICANT: KAPORONT, Basil M.
; TITLE OF INVENTION: "GRAVES" OPHTHALMOPATHY ASSOCIATED
; TITLE OF INVENTION: ANTIBODIES, GRAVES' OPHTHALMOPATHY
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: HALE AND DORR
; STREET: 1455 PENNSYLVANIA AVE., N.W.

```

```

?
? CITY: WASHINGTON,
? STATE: D.C.
? ZIP: 20004
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentln Release #1.0, version #1.25
? CURRENT APPLICATION DATA: 08/124,469
? FILING DATE: 22-SEP-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: MIXON, HENRY N.
? REGISTRATION NUMBER: 32,073
? REFERENCE/DOCKET NUMBER: 102,105,301
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)942-8400
? TELEFAX: (202)942-8400
? INFORMATION FOR SEQ ID NO: 32:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 98 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: Linear
? MOLECULE TYPE: protein
? US-08-124-469-32

Query Match 92.1%; Score 82; DB 5; Length 98;
Best local similarity 88.2%; Pred. No. 8,7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NIKODSEKXYADVSG 17
Db 50 NIKODSEKXYADVSG 66

RESULT 7
US-08-472-771-32
? Sequence 32, Application US/08472771
? GENERAL INFORMATION:
? APPLICANT: RAPOPORT, Basil
? APPLICANT: MCLACHLAN, Sandra M.
? TITLE OF INVENTION: GRAVES' OPTHALMOPATHY ASSOCIATED
? TITLE OF INVENTION: ANTIODIES, GRAVES' OPTHALMOPATHY ORBITAL ANTIGEN,
? NUMBER OF SEQUENCES: 35
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: HALE AND DOHR
? STREET: 1455 PENNSYLVANIA AVE., N.W.
? CITY: WASHINGTON,
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentln Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? FILING DATE: 08/472,771
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/124,469
? NAME: MIXON, HENRY N.
? REGISTRATION NUMBER: 32,073
? REFERENCE/DOCKET INFORMATION:
? TELEPHONE: (202)942-8400
? TELEFAX: (202)942-8400
? INFORMATION FOR SEQ ID NO: 32:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 98 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: Linear
? MOLECULE TYPE: protein
? US-08-472-771-32

```

```

?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 98 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: Linear
? MOLECULE TYPE: protein
? US-08-472-771-32

Query Match 92.1%; Score 82; DB 8; Length 98;
Best local similarity 88.2%; Pred. No. 8,7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NIKODSEKXYADVSG 17
Db 50 NIKODSEKXYADVSG 66

RESULT 8
US-08-486-202-32
? Sequence 32, Application US/08486202
? GENERAL INFORMATION:
? APPLICANT: RAPOPORT, Basil
? APPLICANT: MCLACHLAN, Sandra M.
? TITLE OF INVENTION: GRAVES' OPTHALMOPATHY ASSOCIATED
? TITLE OF INVENTION: ANTIODIES, GRAVES' OPTHALMOPATHY ORBITAL ANTIGEN,
? NUMBER OF SEQUENCES: 35
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: HALE AND DOHR
? STREET: 1455 PENNSYLVANIA AVE., N.W.
? CITY: WASHINGTON,
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentln Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? FILING DATE: 05/08/486,202
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/124,469
? NAME: MIXON, HENRY N.
? REGISTRATION NUMBER: 32,073
? REFERENCE/DOCKET INFORMATION:
? TELEPHONE: (202)942-8400
? TELEFAX: (202)942-8400
? INFORMATION FOR SEQ ID NO: 32:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 98 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: Linear
? MOLECULE TYPE: protein
? US-08-486-202-32

Query Match 92.1%; Score 82; DB 8; Length 98;
Best local similarity 88.2%; Pred. No. 8,7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NIKODSEKXYADVSG 17
Db 50 NIKODSEKXYADVSG 66

RESULT 9
US-09-534-717-664

```

```

: Sequence 664, Application us/09534717
: GENERAL INFORMATION:
: APPLICANT: Jochen, Salteid et al.
: FILE REFERENCE: Human Antibodies That Bind Human IL-12 And Methods For Producing
: CURRENT APPLICATION NUMBER: US/09/534,717
: EARLIER FILING DATE: 2000-03-24
: EARLIER APPLICATION NUMBER: 60/126,603
: NUMBER OF SEQ ID NOS: 675
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 664
: LENGTH: 98
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-534-717-664

```

```

Query Match      92.1%: Score 82; DB 18; Length 98;
Best Local Similarity 88.2%: Pred. No. 8.7e-06;
Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 NIKODSEKRYDVSG 17
        ||||| 11111 |||:|
DB      50 NIKODSEKRYDVSG 66

```

```

RESULT 10
: Sequence 666, Application us/09534717
: GENERAL INFORMATION:
: APPLICANT: Jochen, Salteid et al.
: FILE REFERENCE: Human Antibodies That Bind Human IL-12 And Methods For Producing
: CURRENT APPLICATION NUMBER: US/09/534,717
: EARLIER FILING DATE: 2000-03-24
: EARLIER APPLICATION NUMBER: 60/126,603
: NUMBER OF SEQ ID NOS: 675
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 666
: LENGTH: 98
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-534-717-666

```

```

Query Match      92.1%: Score 82; DB 18; Length 98;
Best Local Similarity 88.2%: Pred. No. 8.7e-06;
Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 NIKODSEKRYDVSG 17
        ||||| 11111 |||:|
DB      50 NIKODSEKRYDVSG 66

```

```

RESULT 11
US-09-751-181-85
: Sequence 85, Application US/09751181
: GENERAL INFORMATION:
: APPLICANT: Bio-Technology General Corp
: FILE REFERENCE: Specific Human Antibodies for Selective Cancer Therapy
: CURRENT APPLICATION NUMBER: US/09/751,181
: EARLIER FILING DATE: 2000-12-29
: NUMBER OF SEQ ID NOS: 202
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 85
: LENGTH: 98
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-751-181-85

```

```

Query Match      92.1%: Score 82; DB 21; Length 98;
Best Local Similarity 88.2%: Pred. No. 8.7e-06;
Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 NIKODSEKRYDVSG 17
        ||||| 11111 |||:|
DB      50 NIKODSEKRYDVSG 66

```

```

RESULT 12
US-08-712-564-10
: Sequence 10, Application US/08712564
: GENERAL INFORMATION:
: APPLICANT: HUNSPREIN, Daniel, R
: TITLE OF INVENTION: HUMAN ANTIBODIES TO CD34
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Baker & Bolls, L.L.P.
: STREET: 1299 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS Compatible
: SOFTWARE USED FOR Windows Version 2.0
: CURRENT APPLICATION NUMBER: US/08/712,564
: FILING DATE: 11-SEP-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: ATTORNEY/AGENT INFORMATION:
: NAME: Posorske, Laurence H
: REGISTRATION NUMBER: 34,698
: REFERENCE/DOCKET NUMBER: 16865-0271
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-639-7700
: TELEFAX: 202-639-7890
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 124 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
US-08-712-564-10

```

```

Query Match      92.1%: Score 82; DB 11; Length 124;
Best Local Similarity 88.2%: Pred. No. 1.2e-05;
Matches 15: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 NIKODSEKRYDVSG 17
        ||||| 11111 |||:|
DB      46 NIKODSEKRYDVSG 62

```

```

RESULT 13
US-60-141-701-75
: Sequence 75, Application US/60141701
: GENERAL INFORMATION:
: APPLICANT: Watkins, Brynmore
: APPLICANT: Reitz, Jr., Marvin
: TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HIV-1 ENVELOPE
: FILE REFERENCE: 2026-4284

```

```

; CURRENT APPLICATION NUMBER: US/60/141,701
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Human Immunodeficiency virus type 1
US-60-141-701-75

```

```

Query Match
Best Local Similarity 82.24; Pred. No. 1.2e-05; Length 125;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 NIKODSEKRYADSVRG 17
Db 51 NIKODSEKRYADSVRG 67

```

```

RESULT 14
US-09-811-737-3
; Sequence 3, Application US/09811737
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human FMT-alpha specific antibodies
; FILE REFERENCE: 1-1129
; CURRENT APPLICATION NUMBER: US/09/811,737
; CURRENT FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-737-3

```

```

Query Match
Best Local Similarity 82.18; Score 82; DB 22; Length 134;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 NIKODSEKRYADSVRG 17
Db 50 NIKODSEKRYADSVRG 66

```

```

RESULT 15
US-09-811-1910-1889
; Sequence 1889, Application PC/US0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that immunospecifically bind blygs
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 212
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1889
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1889

```

```

Query Match
Best Local Similarity 82.18; Score 82; DB 1; Length 241;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 NIKODSEKRYADSVRG 17
Db 50 NIKODSEKRYADSVRG 66

```

```

Search completed: November 19, 2001, 08:23:14
Job time: 727 sec

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 19, 2001, 08:23:31 : Search time 11.44 Seconds

(without alignments) 7.915 Million cell updates/sec

Title: US-09-610-118-62

Sequence: 1 NIKOGSEKRYADSVK 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 25229 segs, 5326477 residues

Total number of hits satisfying chosen parameters: 25229

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 00

Database : Pending Patents AA, New: *

1: /cgn2_6/prodata1/paa/US06_NEW_COMB.pep: *
2: /cgn2_6/prodata1/paa/US06_NEW_COMB.pep: *
3: /cgn2_6/prodata1/paa/US06_NEW_COMB.pep: *
4: /cgn2_6/prodata1/paa/US06_NEW_COMB.pep: *
5: /cgn2_6/prodata1/paa/US06_NEW_COMB.pep: *
6: /cgn2_6/prodata1/paa/US06_NEW_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	71.9	17	5	US-09-972-656-48
2	64	71.9	225	5	US-09-453-234-102
3	64	71.9	225	5	US-09-453-234-106
4	64	71.9	225	5	US-09-453-234-110
5	64	71.9	227	5	US-09-972-656-76
6	63	70.8	179	5	US-09-782-397-2
7	63	70.8	287	5	US-09-782-397-17
8	63	70.8	304	5	US-09-782-397-14
9	62	69.7	17	5	US-09-828-708-24
10	62	69.7	101	5	US-09-828-708-10
11	62	69.7	101	5	US-09-828-708-10
12	61	68.5	102	5	US-09-972-656-126
13	60	67.4	225	5	US-09-453-234-94
14	59	66.3	225	5	US-09-453-234-56
15	59	66.3	225	5	US-09-453-234-60
16	59	66.3	225	5	US-09-453-234-92
17	59	66.3	225	5	US-09-453-234-106
18	59	66.3	225	5	US-09-453-234-106
19	59	66.3	225	5	US-09-453-234-106
20	50	56.2	117	5	US-09-828-708-22
21	50	56.2	117	5	US-09-828-708-8
22	50	56.2	268	1	PCT-US01-31857-1
23	50	56.2	268	5	US-09-976-118-1
24	50	56.2	268	5	US-09-976-118-1
25	47	52.8	17	5	US-09-972-656-45
26	47	52.8	17	5	US-09-972-656-45
27	47	52.8	224	5	US-09-972-656-48

28	47	52.8	225	5	US-09-453-234-68	Sequence 68, Appl
29	47	52.8	230	5	US-09-453-234-64	Sequence 64, Appl
30	47	52.8	368	5	US-09-837-106-136	Sequence 104, Appl
31	47	52.8	368	5	US-09-837-106-136	Sequence 104, Appl
32	47	52.8	368	5	US-09-837-106-136	Sequence 104, Appl
33	45	50.6	102	5	US-09-972-656-123	Sequence 123, Appl
34	45	50.6	102	5	US-09-972-656-127	Sequence 127, Appl
35	45	50.6	220	5	US-09-972-656-78	Sequence 78, Appl
36	45	50.6	463	5	US-09-976-594-721	Sequence 721, Appl
37	43	48.3	225	5	US-09-453-234-92	Sequence 92, Appl
38	43	48.3	225	5	US-09-453-234-92	Sequence 92, Appl
39	43	48.3	225	5	US-09-453-234-92	Sequence 92, Appl
40	42	47.2	115	5	US-09-974-449-2	Sequence 2, Appl
41	41	46.1	218	5	US-09-974-449-35	Sequence 35, Appl
42	40	44.9	102	5	US-09-453-234-62	Sequence 62, Appl
43	40	44.9	102	5	US-09-972-656-125	Sequence 125, Appl
44	40	44.9	225	5	US-09-453-234-58	Sequence 58, Appl
45	40	44.9	225	5	US-09-453-234-66	Sequence 66, Appl
46	40	44.9	225	5	US-09-453-234-98	Sequence 98, Appl

ALIGNMENTS

```

RESULT 1
US-09-972-656-48
: Sequence 68, Application US/09972656
: CURRENT APPLICATION NUMBER: US/09972656
: PRIORITY DATE: 1999-12-01
: APPLICANT: Tsal, Mei-Mei
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: FILE REFERENCE: A-799
: CURRENT APPLICATION NUMBER: US/09972656
: PRIORITY DATE: 1999-12-01
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 48
: LENGTH: 17
: TYPE: PRT
: ORIGIN: Homo sapiens
US-09-972-656-48

Query Match          71.9%  Score 64:  DB 5:  Length 17:
Best Local Similarity 75.0%:  Pred. No. 3.7e+05:
Matches 12:  Conservative 1:  Mismatches 3:  Indels 0:  Gaps 0:

OY      2  NIKOGSEKRYADSVK 17
DB      2  ISYDSNNRYADSVK 17

RESULT 2
US-09-453-234-102
: Sequence 102, Application US/09453234
: CURRENT APPLICATION NUMBER: US/09453234
: PRIORITY DATE: 1999-12-01
: APPLICANT: Walkers, Gunars
: TITLE OF INVENTION: HistoSite Diagnostics, Inc.
: FILE REFERENCE: 020015-000110US
: CURRENT APPLICATION NUMBER: US/09453234
: PRIORITY DATE: 1999-12-01
: NUMBER OF SEQ ID NOS: 112
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 102
: LENGTH: 225
: TYPE: PRT

```


REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-397-2

Query Match 70.8%; Score 63; DB 5; Length 179;
Best Local Similarity 75.0%; Pred. No. 0.00065;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 IKDGSSEKYVADSVG 17
| ||||| ||||| |||||
Db 112 ISYDGSSTYYVADSVKG 127

RESULT 7
US-09-782-397-17
Sequence 14, Application US/09782397
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DIRECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND TREATMENT OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION: K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-782-397-17

Query Match 70.8%; Score 63; DB 5; Length 287;
Best Local Similarity 75.0%; Pred. No. 0.0011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 IKDGSSEKYVADSVG 17
| ||||| ||||| |||||
Db 193 ISYDGSSTYYVADSVKG 208

RESULT 8
US-09-782-397-14
Sequence 14, Application US/09782397
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DIRECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND TREATMENT OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-782-397-14

Query Match 70.8%; Score 63; DB 5; Length 304;
Best Local Similarity 75.0%; Pred. No. 0.0011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 IKDGSSEKYVADSVG 17
| ||||| ||||| |||||
Db 210 ISYDGSSTYYVADSVKG 225

RESULT 9
US-09-828-708-24
Sequence 24, Application US/09828708
GENERAL INFORMATION:
APPLICANT: Ditzel, H.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:13:24 ; Search time 43.5 Seconds
(without alignments)
8.794 Million cell updates/sec

Title: US-09-610-118-62

Sequence: 1 NIKODSEKRYADSVNG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scanned: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA*
1: /cgn2_6/p/odata/2/1aa/5a.COMB.pep.*
2: /cgn2_6/p/odata/2/1aa/5a.COMB.pep.*
3: /cgn2_6/p/odata/2/1aa/6a.COMB.pep.*
4: /cgn2_6/p/odata/2/1aa/6a.COMB.pep.*
5: /cgn2_6/p/odata/2/1aa/6a.COMB.pep.*
6: /cgn2_6/p/odata/2/1aa/backlist.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	82	92.1	98	1	US-07-942-245-37	Sequence 37, Appl
2	82	92.1	98	1	US-08-545-809A-95	Sequence 13, Appl
3	69	73.5	116	3	US-08-545-809A-134	Sequence 13, Appl
4	69	73.5	116	3	US-08-545-809A-134	Sequence 13, Appl
5	69	73.5	116	3	US-08-545-809A-134	Sequence 13, Appl
6	65	73.0	126	1	US-08-478-039-95	Sequence 95, Appl
7	65	73.0	126	1	US-08-478-039-95	Sequence 95, Appl
8	64	71.9	98	1	US-08-211-202-118	Sequence 118, Appl
9	64	71.9	116	1	US-08-211-202-141	Sequence 141, Appl
10	64	71.9	117	3	US-08-545-809A-115	Sequence 115, Appl
11	64	71.9	117	3	US-08-545-809A-115	Sequence 115, Appl
12	64	71.9	119	4	US-08-331-392A-46	Sequence 46, Appl
13	64	71.9	119	4	US-08-331-392A-46	Sequence 46, Appl
14	64	71.9	119	4	US-08-331-392A-46	Sequence 46, Appl
15	64	71.9	120	1	US-08-211-202-135	Sequence 135, Appl
16	64	71.9	120	1	US-07-942-245-35	Sequence 35, Appl
17	64	71.9	123	1	US-08-983-607-38	Sequence 38, Appl
18	64	71.9	123	1	US-08-983-607-38	Sequence 38, Appl
19	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl
20	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl
21	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl
22	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl
23	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl
24	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl
25	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl
26	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl
27	64	71.9	125	1	US-08-276-852-72	Sequence 72, Appl

28	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
29	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
30	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
31	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
32	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
33	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
34	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
35	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
36	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
37	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
38	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
39	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
40	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
41	64	71.9	125	1	US-08-899-575-76	Sequence 76, Appl
42	64	71.9	128	1	US-08-478-039-96	Sequence 96, Appl
43	64	71.9	128	1	US-08-478-039-96	Sequence 96, Appl
44	63	70.8	179	4	US-08-852-124-17	Sequence 2, Appl
45	63	70.8	287	4	US-08-852-124-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-07-942-245-37
Sequence 37, Appl
PCT-US95-08743-72
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: RUTLO, Jeffrey
TITLE OF INVENTION: SEQUENCE RESIDUE VENERING OF ROBERT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sughture, Mion, 21m, Nappeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT STATUS: IN DATA
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 645453
INVENTOR: ROBERTSON, J.D.
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-37
Query Match 92.1% Score 82: DB 1: Length 98:
Best Local Similarity 88.2% Pred. No. 36-07:
Matches 15: Conservative 1: Mismatches 1: Indels 0: Gaps 0:
DB 50 NIKODSEKRYADSVNG 66

```

RESULT 2
US-08-545-809A-95
Sequence 95, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasaku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF INVENTION: SEQUENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENTS: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545.809A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
ADDRESS: 116 amino acids
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 117
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-95

Query Match
Best Local Similarity 92.1%, Score 82, DB 3, Length 117:
Matches 15: Conservative 1, Mismatches 1, Indels 0, Gaps 0:

DB 69 NIKDGSSEKRYVDSVG 85

RESULT 3
US-08-545-809A-134
Sequence 134, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasaku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF INVENTION: SEQUENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545.809A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
ADDRESS: 116 amino acids
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 116
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-134

Query Match
Best Local Similarity 76.5%, Score 69, DB 3, Length 116:
Matches 13: Conservative 2, Mismatches 2, Indels 0, Gaps 0:

DB 68 DDKDGSSEKRYVDSVG 84

RESULT 4
US-09-240-274-141
Sequence 141, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: METHOD OF CLONING PROTEINS AND MANIPULATING ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240.274
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION DATA:
EARLIER APPLICATION NUMBER: 60/091,380
EARLIER FILING DATE: 1998-04-10
EARLIER PRIORITY NUMBER: 60/078,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 141
LENGTH: 117
TYPE: RT
FEATURE: Homo sapiens
OTHER INFORMATION: anti-Rh(D) antibody clone SH12
US-09-240-274-141

Query Match
Best Local Similarity 75.3%, Score 67, DB 4, Length 117:
Matches 13: Conservative 1, Mismatches 3, Indels 0, Gaps 0:

DB 50 NIKDGSSEKRYVDSVG 66

RESULT 5
US-08-545-809A-124

```

```

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545.809A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
ADDRESS: 116 amino acids
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 116
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-134

Query Match
Best Local Similarity 75.3%, Score 69, DB 3, Length 116:
Matches 13: Conservative 2, Mismatches 2, Indels 0, Gaps 0:

DB 68 DDKDGSSEKRYVDSVG 84

RESULT 4
US-09-240-274-141
Sequence 141, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: METHOD OF CLONING PROTEINS AND MANIPULATING ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240.274
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION DATA:
EARLIER APPLICATION NUMBER: 60/091,380
EARLIER FILING DATE: 1998-04-10
EARLIER PRIORITY NUMBER: 60/078,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 141
LENGTH: 117
TYPE: RT
FEATURE: Homo sapiens
OTHER INFORMATION: anti-Rh(D) antibody clone SH12
US-09-240-274-141

Query Match
Best Local Similarity 75.3%, Score 67, DB 4, Length 117:
Matches 13: Conservative 1, Mismatches 3, Indels 0, Gaps 0:

DB 50 NIKDGSSEKRYVDSVG 66

RESULT 5
US-08-545-809A-124

```

```

: Sequence 124, Application US/08545809A
: Patent No. 6096878
: GENERAL INFORMATION:
: APPLICANT: HONJO, TOSIKU
: APPLICANT: HONJO, TOSIKU
: TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
: NUMBER OF SEQUENCES: 145
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.
: STREET: 225 Franklin Street
: STATE: Boston
: COUNTRY: US
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: ISDOSE/MS-DOS Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/545,809A
: FILING DATE: 27-MAR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP93/00603
: FILING DATE: 10-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: W 29,066
: REFERENCE/DOCKET NUMBER: 06501/004001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-542-5070
: TELEFAX: 617-542-8906
: TELEX: 200124
: INFORMATION FOR SEQ ID NO: 124:
: STRANDEDNESS: not relevant
: TYPE: amino acid
: LENGTH: 114 amino acids
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-545-809A-124

Query Match          73.0% Score 65; DB 3; Length 114;
Best Local Similarity 70.6% Pred. No. 0.00033;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY      1 NIKDSEKRYADSYNG 17
DB      68 HAMDOSRFTADSYNG 84

```

```

: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/478,039
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/379,072
: FILING DATE: 25-JAN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/912,292
: FILING DATE: 23-MAR-1992
: APPLICATION NUMBER: US/07/856,281
: FILING DATE: 23-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/735,064
: FILING DATE: 25-JUL-1991
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: W 29,066
: REFERENCE/DOCKET NUMBER: 012712-160
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-6620
: INFORMATION FOR SEQ ID NO: 95:
: STRANDEDNESS: not relevant
: TYPE: amino acid
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT: RF S31
: US-08-478-039-95

Query Match          73.0% Score 65; DB 1; Length 126;
Best Local Similarity 75.0% Pred. No. 0.00036;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      2 IKDSEKRYADSYNG 17
DB      51 ISDSEKRYADSYNG 66

RESULT 7
US-08-476-349A-95
: Sequence 95, Application US/08476349A
: Patent No. 5701025
: GENERAL INFORMATION:
: APPLICANT: Neuman, Roland A.
: APPLICANT: Haehn, Nobli W.
: TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
: NUMBER OF SEQUENCES: 114
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOWNE, SWECKER & MATHIS
: STREET: 699 Prince St.
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: PC-DOS/MS-DOS
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/476,349A
: FILING DATE: 07-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/379,072

```

FILED DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 2811/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
US-08-476-343h-95

Query Match
Best Local Similarity 73.0%; Score 65; DB 1; Length 126;
Matches 12: Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 2 IKDDSKRYADSVK 17
51 ISDGSNKYYADSVK 66

RESULT 8
US-08-211-202-118
Sequence 118: Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAILEY, Michael
APPLICANT: JESPERSEN, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
500 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120352.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 2811/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-211-202-118

Query Match
Best Local Similarity 71.9%; Score 64; DB 1; Length 98;
Matches 12: Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 2 IKDDSKRYADSVK 17
51 ISDGSNKYYADSVK 66

RESULT 9
US-08-211-202-141
Sequence 141: Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAILEY, Michael
APPLICANT: JESPERSEN, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
500 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120352.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA: C/T/03892/00883
 APPLICATION NUMBER: 1355 MAY 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 INFORMATION FOR SEQ ID NO: 141:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-211-202-141

Query Match 71.9%; Score 64; DB 1; Length 116;
 Best Local Similarity 75.0%; Pred. No. 0.0005;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 IKODSEKRYADSVRG 17
 Db 51 ISYDSNNYADSVRG 66

RESULT 10
 US-08-543-809A-115
 Sequence 46, Application US/08545809A
 Patent No. 6096878
 GENERAL INFORMATION:
 APPLICANT: Honjo, Tasuku
 APPLICANT: Malsuda, Fumihiko
 TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
 NUMBER OF SEQUENCES: 15
 NUMBER OF INVENTORS: 15
 ADDRESSER: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Fastsed for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/545, 809A
 FILING DATE: 27-MAR-1996
 PENDING APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP93/00603
 FILING DATE: 10-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Freeman, John W.
 REGISTRATION NUMBER: 29,066
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8606
 INFORMATION FOR SEQ ID NO: 115:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-545-809A-115

Query Match 71.9%; Score 64; DB 3; Length 117;
 Best Local Similarity 75.0%; Pred. No. 0.0005;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 IKODSEKRYADSVRG 17
 Db 70 ISYDSNNYADSVRG 85

RESULT 11
 US-08-331-398A-46
 Sequence 46, Application US/08331398A
 Patent No. 5608039
 GENERAL INFORMATION:
 APPLICANT: Millingham, Mark
 APPLICANT: Fitzgerald, David
 APPLICANT: Brinkmann, Ulrich
 APPLICANT: Pal, Lee
 TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
 TITLE OF INVENTION: and Their Uses (as amended)
 NUMBER OF SEQUENCES: 60
 ADDRESSER: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Street Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-4102
 COMPUTER: PLOPPY disk
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/331, 398A
 FILING DATE: 30-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 30-SEP-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-9643
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 EXPLAN/KEY:
 LOCATION: 1..119
 OTHER INFORMATION: 56P1.C1 Variable Heavy chain (V-H)*
 US-08-331-398A-46

Query Match 71.9%; Score 64; DB 1; Length 119;
 Best Local Similarity 75.0%; Pred. No. 0.0005;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

01 2 IKODSEKYYADSVRG 17
02 1 ||| |||||:|
03 51 ISYDSKMYADSVK 66

RESULT 12
US-08-331-3978-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
INVENTOR: Benhar, Itai
TITLE OF INVENTION: Specific and Mutationally Stabilized Tumor-
SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-5193
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331.397B
CLASSIFICATION:
PRIORITY: 46
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION:
OTHER INFORMATION: 50p1C1 Variable Heavy chain (V-H)*
US-08-331-3978-46

Query Match 71.9% Score 64; DB 2; Length 119;
Best Local Similarity 75.0% Pred. NO. 0.00051;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
01 2 IKODSEKYYADSVRG 17
02 1 ||| |||||:|
03 51 ISYDSKMYADSVK 66

RESULT 13
US-08-759-804A-46
Sequence 46, Application US/08759804A

```

```

? Patent No. 5990296
? GENERAL INFORMATION:
? APPLICANT: Pastan, Ira
? APPLICANT: Berman, Mark
? APPLICANT: Flitzberg, David J.
? APPLICANT: Brinkmann, Ulrich
? APPLICANT: Pal, Lee
? TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
? TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
? NUMBER OF SEQUENCES: 68
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dr. Joseph and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIA TYPE: Floppy disk
? COMPUTER SOFTWARE COMPATIBLE
? OPERATING SYSTEM: MSDOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/759,804A
? FILING DATE: 03-DEC-1996
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? PRIOR APPLICATION NUMBER: US 08/331,398
? FILING DATE: 02-OCT-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/767,331
? FILING DATE: 30-SEP-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/596,289
? FILING DATE: 12-OCT-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Weber, Elizabeth
? REGISTRATION NUMBER: L 32,762
? REFERENCE/DOCKET NUMBER: 015280-126140US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO. 46:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 119 amino acids
? TYPE: amino acid
? STRANDEDNESS: 1
? TOPOLOGY: linear
? FEATURE:
? MOLECULE TYPE: protein
? DISORDER: protein
? LOCATION: 1
? OTHER INFORMATION: /note="Human fetal immunoglobulin"
? OTHER INFORMATION: 56P1CL Variable Heavy chain (Y-H)"
? US-08-759-804A-46

```

```

1  APPLICANT: RADIAN, Eduardo A.
2  APPLICANT: LEE, Bruce Lee
3  APPLICANT: LEE, Bruce Lee
4  TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
5  TITLE OF INVENTION: FRAGMENTED, FUSION PROTEINS, AND USES THEREOF
6  NUMBER OF SEQUENCE ADDRESSES: 50
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Townsend and Townsend Knourie and Crew
9  STREET: Stewart Street Tower, One Market Plaza
10 CITY: San Francisco
11 STATE: California
12 COUNTRY: US
13 ZIP: 94105-1493
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: IBM PC compatible
17 SOFTWARE: Patent In Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/227,693
20 FILING DATE:
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/331,396
23 FILING DATE:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/767,331
26 FILING DATE: 30-SEP-1991
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/596,289
29 FILING DATE: 12-OCT-1990
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Weber, Ellen Lauever
32 FIRM: WEBER, ELLEN LAUEVER
33 REFERENCE/DOCKET NUMBER: 915280-126-1-3
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (415) 543-9600
36 TELEFAX: (415) 543-9603
37 INFORMATION FOR SEQ ID NO: 46:
38 SEQUENCE CHARACTERISTICS:
39 TYPE: amino acids
40 STRANDEDNESS: ds1single
41 TOPOLOGY: linear
42 MOLECULE TYPE: peptide
43 FEATURE:
44 NAME/KEY: Protein
45 LOCATION: 1..119
46 OTHER INFORMATION:
47 OTHER INFORMATION: 50P1 CL YA region
48
49 US-09-227-693-46
50
51 Query Match
52 Best Local Similarity 71.9%; Score 64; DB 4; Length 119:
53 Matches 12: Conservative 1; Mismatches 3; Indels 0; Gaps 0:
54
55 QY 2 IKDDSKRYADSVRG 17
56 | ||| |||||
57 DB 51 ISYDGNKRYADSVRG 66
58
59 RESULT 15
60 US09-211-202-135
61 Sequence 135: Application US/08211202
62 Patent No. 5565332
63 GENERAL INFORMATION:
64 APPLICANT: HOOGERBOM, Hendricus Renerus Jacobus Matheus
65 APPLICANT: BATES, Michael
66 APPLICANT: JESPER, Laurence Stephane Anne Therese
67 APPLICANT: JESPER, Gregoire Paul
68 TITLE OF INVENTION: Generation of chimeric antibodies - a
69 TITLE OF INVENTION: combinatorial approach
70 NUMBER OF SEQUENCES: 144

```

```

1  CORRESPONDENCE ADDRESS:
2  ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
3  STREET: 3400 Sears Tower, 233 South Wacker Drive
4  CITY: Chicago
5  STATE: Illinois
6  COUNTRY: USA
7  ZIP: 60606-6402
8  COMPUTER READABLE FORM:
9  MEDIUM TYPE: Floppy disk
10 OPERATING SYSTEM: IBM PC compatible
11 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/211,202
14 FILING DATE: 23-SEP-1992
15 CLASSIFICATION: 435
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: GB 9120252.3
18 FILING DATE: 23-SEP-1991
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: GB 9120377.8
21 FILING DATE: 25-SEP-1991
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: GB 9206318.9
24 FILING DATE: 24-MAR-1992
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: GB 9206372.6
27 FILING DATE: 24-MAR-1992
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: PCT/GB92/00883
30 FILING DATE: 15-MAY-1992
31 ATTORNEY/AGENT INFORMATION:
32 NAME: David W. Clough
33 FIRM: DWM CLOUGH
34 REFERENCE/DOCKET NUMBER: 128111/31960
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 312-474-6300
37 TELEFAX: 312-474-0448
38 INFORMATION FOR SEQ ID NO: 135:
39 SEQUENCE CHARACTERISTICS:
40 TYPE: amino acids
41 STRANDEDNESS: ds1single
42 TOPOLOGY: linear
43 MOLECULE TYPE: protein
44
45 US-08-211-202-135

```

```

1  Query Match
2  Best Local Similarity 71.9%; Score 64; DB 1; Length 120:
3  Matches 12: Conservative 1; Mismatches 3; Indels 0; Gaps 0:
4
5  QY 2 IKDDSKRYADSVRG 17
6 | ||| |||||
7 DB 51 ISYDGNKRYADSVRG 66

```

Search completed: November 19, 2001, 08:13:24
Job time: 137 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: November 19, 2001, 08:14:20 : Search time 48.99 Seconds

(without alignments)
21.765 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 1.00

Sequence: 1 DKMFAYITPCADV 14

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Hit 1008

Listing first 45 summaries

Database :

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	57.5	48.4	2	T38463	probable amnuron
2	56.2	76.5	2	S76795	hypothetical prote
3	55.0	17.5	2	T00186	cdtr pyrophosphata
4	55.0	68.2	2	T50840	U4/66 small nuclea
5	55.0	68.3	2	T50839	hypothetical prote
6	55.0	68.3	2	T50839	hypothetical prote
7	55.0	86.9	2	E85553	partial fibrial u
8	53.8	65.3	2	E85620	partial fibrial u
9	53.8	86.6	1	C64834	probable outer mem
10	52.5	10.8	2	PH1015	1g heavy chain V r
11	51.2	31.2	2	E71624	1g heavy chain V r
12	51.2	31.2	2	E71624	1g heavy chain V r
13	51.2	37.8	2	T50761	alpha-galactosidas
14	51.2	37.8	2	T50761	alpha-galactosidas
15	51.2	40.2	2	T50761	alpha-galactosidas
16	51.2	48.2	2	T06368	alpha-galactosidas
17	51.2	68.2	2	H82296	cd-cl-dmp phosphol
18	51.2	79.6	2	T23238	hypothetical prote
19	50.0	7.21	2	C71014	hypothetical prote
20	50.0	31.58	2	T17483	peptide synthetase
21	48.8	14.8	2	E71267	hypothetical prote
22	48.8	14.8	2	E71267	hypothetical prote
23	48.8	36.7	2	A86029	hypothetical prote
24	48.8	36.7	2	A86029	hypothetical prote
25	48.8	43.4	2	T47748	alpha-galactosidas
26	48.8	49.5	2	G83325	probable sulfatase
27	48.8	59.2	2	PS0197	phospholipase C (E
28	48.8	59.2	2	PS0197	phospholipase C (E
29	48.8	59.2	2	PS0197	phospholipase C (E
30	48.8	59.2	2	PS0197	phospholipase C (E
31	48.8	59.2	2	PS0197	phospholipase C (E
32	48.8	59.2	2	PS0197	phospholipase C (E
33	48.8	59.2	2	PS0197	phospholipase C (E
34	48.8	59.2	2	PS0197	phospholipase C (E
35	48.8	59.2	2	PS0197	phospholipase C (E
36	48.8	59.2	2	PS0197	phospholipase C (E
37	48.8	59.2	2	PS0197	phospholipase C (E
38	48.8	59.2	2	PS0197	phospholipase C (E
39	48.8	59.2	2	PS0197	phospholipase C (E
40	48.8	59.2	2	PS0197	phospholipase C (E
41	48.8	59.2	2	PS0197	phospholipase C (E
42	48.8	59.2	2	PS0197	phospholipase C (E
43	48.8	59.2	2	PS0197	phospholipase C (E
44	48.8	59.2	2	PS0197	phospholipase C (E
45	48.8	59.2	2	PS0197	phospholipase C (E

ALIGNMENTS

30	39	48.8	1041	2	E70760	probable 11S prot
31	38	47.5	1041	2	E70760	probable 11S prot
32	38	47.5	1041	2	E70760	probable 11S prot
33	38	47.5	133	2	PC1155	hypothetical prote
34	38	47.5	204	2	T04423	probable alpha-gal
35	38	47.5	257	2	H84597	hypothetical prote
36	38	47.5	288	2	D82892	conserved hypotet
37	38	47.5	328	2	H84545	hypothetical prote
38	38	47.5	349	2	C72630	probable theonell
39	38	47.5	349	2	C72630	probable theonell
40	38	47.5	442	2	B51180	antibiotic/peptide
41	38	47.5	482	2	CJ7332	endoglycosylceram
42	38	47.5	656	2	T28058	hypothetical prote
43	38	47.5	659	2	C85057	probable receptor
44	38	47.5	756	2	S67433	hypothetical prote
45	38	47.5	1218	2	S71376	glutamate receptor

RESULT 1
T38463
Probable aminotransferase (EC 2.6.1.-) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Accession: T38463
C:Accession: T38463
R:Harriis, D.; McDonald, S.; Batirelli, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: 221794
A:Accession: T38463
A:Status: preliminary; translated from GH/EMBL/DBJ
A:Molecule type: DNA
A:Accession: T38463
A:Cross-references: EMBL:Z69368; PDB:CM93294.1; GSPDB:GN00066; SPDB:SPAC27F1.05c
A:Experimental source: strain 97zh; cosmid c27F1
C:Genetics:
A:Gene: SPDB:SPAC27F1.05c
A:Map position: 1
C:Superfamily: beta-alanine-pyruvate transaminase
C:Keywords: aminotransferase

Query Match 57.5%; Score 46; DB 2; Length 484;
Best Local Similarity 50.0%; Pred. No. 3.6;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 DKMFAYITPCADV 14

DB 204 ERMKXGSHAPDV 217

RESULT 2
S76795
Hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
C:Accession: S76795
C:Accession: S76795
C:Date: 75-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

R:Kinako, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the uncultured cyanobacterium Synecocys
A:Reference number: S74322; MIMD:97061201
A:Accession: S76795
A:Status: preliminary
A:Molecule type: RNA
A:Residues: 1-765 <RNA>
A:Cross-references: EMBL:D90916; GB:AB01139; MIMD:91653715; PDB:1BA18707.1; PDB:4101

A>Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

RESULT 5
T50839.
U4/Y5 small nuclear ribonucleoprotein hprp3 [imported] - human
C.Species: Homo sapiens (man)
C.Date: 21-Jul-2000 #sequence-revision 21-Jul-2000 #text-change 21-Jul-2000

A:status: preliminary
A:molecule_type: DNA
A:residues: 1-865 (>570)
A:Cross-references: GB:AE005174; NID:J12513432; PTDN:AG654889.1; GSPPB:GNO0145; UNKCP:
A:Experimental source: strain 0157:H7, substrain EDL933
C:Genetics:

A:Reference number: 225235; MUID:94193002
 A:Accession: T50781
 A:Species: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: protein
 A:Residues: 1378 <NH>
 A:Cross-references: EMBL:L27992; PIDD:MAA3022.1
 C:Superfamily: alpha-galactosidase
 C:Keywords: glycosidase; hydrolase

Query Match
 Best Local Similarity 51.2%; Score 41; DB 2; Length 378;
 46.2%; Pred. No. 20;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 DKWEAYITPGAFD 13
 111 : 111 : :

DB 216 DKMASTACPGGN 228

RESULT 13

A:75328
 A:Title: Phb-related protein - *Delnoccocus radiodurans* (strain R1)
 C:Species: *Delnoccocus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: AF5328
 A:Molecule type: protein
 A:Residues: 1378 <NH>
 A:Cross-references: EMBL:U12976; MUID:9527574; PIDD:MAA31963.1; PID:9927575
 A:Functional source: strain Williams
 A:Description: catalyzes hydrolysis of malibiose into galactose and glucose
 C:Superfamily: alpha-galactosidase
 C:Keywords: glycosidase; hydrolase
 A:Accession: AF5328
 A:Title: Genome sequence of the radioreistant bacterium *Delnoccocus radiodurans* R1.
 A:Reference number: A55250; MUID:2003696
 A:Accession: AF5328
 A:Species: Preliminary
 A:Molecule type: protein
 A:Residues: 1380 <NH>
 A:Cross-references: GB:AE002038; GB:AE005513; MUID:96459790; PIDD:AAPI1540.1; PID:9645977
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1988
 A:Map position: 1
 C:Superfamily: phosphate starvation-induced protein

Query Match
 Best Local Similarity 51.2%; Score 41; DB 2; Length 380;
 42.9%; Pred. No. 20;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 DKWEAYITPGAFD 14
 111111 : 111111 : :

DB 243 EKFEAYITSCVIEI 256

RESULT 14

A:507472
 A:Title: alpha-galactosidase (EC 3.2.1.22) precursor - guar
 C:Species: *Cyamopsis tetragonoloba* (Guar) - *Cyamopsis*
 C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 22-Jun-1999
 C:Accession: S07472
 R:Overbeek, N.; Fellinger, A.J.; Toonen, M.Y.; van Wassenaar, D.; Veerips, C.T.
 Plant Mol. Biol. 13, 541-550, 1989
 A:Title: Cloning and nucleotide sequence of the alpha-galactosidase cDNA from *Cyamopsis*
 A:Reference number: S07472; MUID:91370836
 A:Accession: S07472
 A:Molecule type: mRNA
 A:Residues: 1-411 <CV>
 A:Cross-references: EMBL:M1619; MUID:q18291; PIDD:CAA32772.1; PID:q18292
 A:Note: The authors translated the codon ATT for residue 20 as Asn, TAT for residue 140
 C:Superfamily: alpha-galactosidase
 C:Keywords: glycosidase; hydrolase

Query Match
 Best Local Similarity 51.2%; Score 41; DB 2; Length 411;
 46.2%; Pred. No. 22;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 DKWEAYITPGAFD 13
 111 : 111 : :

DB 248 DKMASTACPGGN 260

RESULT 15

A:706388
 A:Title: alpha-galactosidase (EC 3.2.1.22) - soybean
 C:Species: Glycine max (soybean)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Jun-1999
 C:Accession: T06388
 A:Molecule type: protein
 A:Residues: 1422 <DA>
 A:Cross-references: EMBL:M12976; MUID:9927574; PIDD:MAA31963.1; PID:9927575
 A:Functional source: strain Williams
 A:Description: catalyzes hydrolysis of malibiose into galactose and glucose
 C:Superfamily: alpha-galactosidase
 C:Keywords: glycosidase; hydrolase
 A:Accession: T06388
 A:Title: alpha-galactosidase (EC 3.2.1.22) - soybean
 C:Species: Glycine max (soybean)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Jun-1999
 C:Accession: T06388
 A:Molecule type: protein
 A:Residues: 1422 <DA>
 A:Cross-references: EMBL:M12976; MUID:9927574; PIDD:MAA31963.1; PID:9927575
 A:Functional source: strain Williams
 A:Description: catalyzes hydrolysis of malibiose into galactose and glucose
 C:Superfamily: alpha-galactosidase
 C:Keywords: glycosidase; hydrolase

Query Match
 Best Local Similarity 51.2%; Score 41; DB 2; Length 422;
 46.2%; Pred. No. 22;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 DKWEAYITPGAFD 13
 111 : 111 : :

DB 260 DKMASTACPGGN 272

Search completed: November 19, 2001, 08:14:21
 Job time: 194 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:25:34 : Search time 27.32 Seconds

(Without alignments) 17,554 Million cell updates/sec

Title: US-09-610-118-63

Sequence: 1 DKMEATITPCAFDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : SwissProt_39.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	57.5	484	1	YAW3_SCHRO
2	46	55.0	867	1	SRND_ECOLI
3	44	55.0	867	1	SRND_ECOLI
4	44	51.2	378	1	AGAL_COCHR
5	41	51.2	411	1	AGAL_COCHR
6	41	51.2	411	1	AGAL_COCHR
7	40	50.0	870	1	YRS7_CAREL
8	39	48.8	283	1	PHIC_SALTY
9	39	48.8	283	1	PHIC_SALTY
10	39	48.8	283	1	PHIC_SALTY
11	39	48.8	283	1	PHIC_SALTY
12	38	47.5	109	1	Y030_MYCVU
13	38	47.5	109	1	Y030_MYCVU
14	38	47.5	109	1	Y030_MYCVU
15	38	47.5	109	1	Y030_MYCVU
16	38	47.5	109	1	Y030_MYCVU
17	38	47.5	109	1	Y030_MYCVU
18	38	47.5	109	1	Y030_MYCVU
19	38	47.5	109	1	Y030_MYCVU
20	38	47.5	109	1	Y030_MYCVU
21	38	47.5	109	1	Y030_MYCVU
22	38	47.5	109	1	Y030_MYCVU
23	38	47.5	109	1	Y030_MYCVU
24	38	47.5	109	1	Y030_MYCVU
25	38	47.5	109	1	Y030_MYCVU
26	38	47.5	109	1	Y030_MYCVU
27	38	47.5	109	1	Y030_MYCVU
28	38	47.5	109	1	Y030_MYCVU
29	38	47.5	109	1	Y030_MYCVU
30	38	47.5	109	1	Y030_MYCVU
31	38	47.5	109	1	Y030_MYCVU
32	38	47.5	109	1	Y030_MYCVU
33	38	47.5	109	1	Y030_MYCVU

34	36	45.0	584	1	PMEL_CITSI
35	36	45.0	666	1	POL_FMDV
36	36	45.0	666	1	POL_FMDV
37	36	45.0	666	1	POL_FMDV
38	36	45.0	666	1	POL_FMDV
39	36	45.0	666	1	POL_FMDV
40	36	45.0	666	1	POL_FMDV
41	36	45.0	666	1	POL_FMDV
42	36	45.0	666	1	POL_FMDV
43	36	45.0	666	1	POL_FMDV
44	36	45.0	666	1	POL_FMDV
45	36	45.0	666	1	POL_FMDV

ALIGNMENTS

RESULT 1
XN3_CITPO
11 YAW3_SCHRO STANDARD: PRT: 484 AA.
AC 010174:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PROBABLE AMINOTRANSFERASE C27H105C (EC 2.6.1.-).
DN SRA27271.1 Schistosoma pombe (Pisition yeast).
OC Schistosoma pombe (Pisition yeast).
OC Eukaryota: Fungi: Ascomycota: Schistosomycetaceae;
OC Schistosomycetaceae: Schistosomycetaceae;
OC Schistosomycetaceae: Schistosomycetaceae;
OC NCBI_TaxID=496;
BN (1)
RP SEQUENCE FROM N.A.
RP Schistosoma pombe (Pisition yeast).
RP Harris D, McDonald S, Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
CC -1- COPOLYMER: PYRIDOXAL PHOSPHATE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC THIS SWISS-PROT entry is a copy-right. It is produced through a collaboration
CC between the Institute of Bioinformatics and the EMBL outstation.
CC The European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announcel/>
CC or send an email to license@isb-sib.ch).
CC -----
CC P03168: CNA9294.1;
CC DR Schistosoma pombe (Pisition yeast).
CC DR InterPro: IPR000954;
CC DR Pfam: PF00202; Anticodon 3; 1.
CC DR PROSITE: PS00600; AA: TRANSFER: 3; 1.
CC KW Hypothetical protein: Transferase: Anticodontransferase;
CC PYRIDOXAL PHOSPHATE.
CC FT BINDING 305
CC SQ SEQUENCE 484 AA; 53190 MW; 5085158A35C97 CRC64.
Query Match 57.5% Score 46; DB 1; Length 484;
Best Local Similarity 50.0% Prod. No. 2;
Matches 7; Conservative 3; Mismatches 4; Gaps 0;
DB 1 DKMEATITPCAFDV 14
204 EKNXKYSAPAPDV 217
OY
RESULT 2
SFND_ECOLI STANDARD: PRT: 867 AA.
ID SFND_ECOLI
CC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

	Best Local Similarity	41.7%	Pred. No.	37;			
	Matches	5;	Conservative	6; Mismatches	1; Indels	0; Gaps	0;
Qy	3 WEATIPGADP	14	::::: ;				
Db	310 YOSYSPGPAPL	321					
 RESULT 8 PHLC_BACCE							
ID	PHLC_BACCE	STANDARD:	PRG:	283 AA.			
AC	P09598:						
DT	01-MAR-1989 (Rel. 10, Created)						
DT	01-MAR-1989 (Rel. 10, Last sequence update)						
DT	15-OCT-1998 (Rel. 37, Last annotation update)						
DE	PROHIDRASE C. FRECHONOR (EC 3.1.14.3) (PLC) (PHOSPHATIDYLCHOLINE CHOLINEROSTROPHIONOLAN), (GENEOLYSIN N).						

CC Bacillus thuringiensis; Bacillus/Clostridium group;
OC Bacillus/streptococcus group; Bacillus.
OX NCBI_taxid=1396.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SE-1;
RX MEDLINE=88313678;. PubMed=3137122;
RT Johansen T., Holm T., Guddal P.H., Stelten K., Haugli F.B., Little C.;
RT Cloning and sequencing of the gene encoding the phosphatidylcholine
RT prefering phospholipase C of *Bacillus cereus*?;
RN Pubmed 051235-504(11968).
RP SEQUENCE FROM N.A.
RC STRAIN-VKM 164;
RX MEDLINE=93249510;. PubMed=8387306;
RT Kuzina N.P., Gavrilchenko I.V., Krivkov V.M., Karpov A.V.;
RT Nucleotide sequence of phosphatidylphosphatase C and sphingomyelinase genes
RT from *Bacillus cereus* BM-B166 [letter].?
RL Bioorg. Khim. 19:133-136(1993).
RN [1]
RP SEQUENCE OF 16S-283 FROM N.A.
RC STRAIN-TM 1208;
RX MEDLINE=88236483;. PubMed=2841128;
RT Yamada A.C., Tsukagoshi N., Ueda S., Sasaki T., Makino S., Nakamura S.,
RT Little C., Tomikoshi M., Ikezawa H.;
RT Nucleotide sequence and expression in *Escherichia coli* of the gene
RT coding for sphingomyelinase of *Bacillus cereus*?;
RL Eur. J. Biochem. 175:213-220(1988).
RN [4]
RP SEQUENCE OF 39-65.
RC MEDLINE=76043151;. PubMed=72664;
RT O'Brien A.D., Priddy H.C., Stetten K., Wallin R., Johnson S.,
RT Flomberg B., Prydz H.C.;
RP Some characteristics of phospholipase C from *Bacillus cereus*?;
RN Eur. J. Biochem. 79:459-468(1977).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=89159438;. PubMed=2493587;
RT Hough E., Hansen L.R., Birkenes B., Jynge K., Hansen S., Hordvik A.,
RT Little C., Dodson E., Deweeds Z.;
RT High resolution (1.5 Å) crystal structure of phospholipase C from
RN Nature 338:357-360(1998).
RP -1 FUNCTION: REMOVED.
RX LYSIN (HEMOXYLIS).
RP -1 CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H₂O → 1,2-DIACYLGlycerol + CHOLINE PHOSPHATE.
RP -1 COFACTOR: THREE ZINC IONS.
RP -1 SUBUNIT: MONOMER.
RP -1 SIMILARITY: TO BETA-HEMOLYSIN OF STREPTOCOCCUS AUREUS.
RP This SwissProt entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Centre/Harwell.

```

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.lsb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
CC EMBL: X6411: CAA45502.1
CC EMBL: X12554: CAA31332.1
CC EMBL: X12711: CAA31213.1
CC EMBL: X64140: CAA45501.1; ALT-TERM.
CC PIR: S03200; S03200.
CC PIR: S01949; S01949.
CC PIR: IAH7; I0-DEC-97.
CC PIR: P00882; P00882.
CC PRINTS: P00479; P00479.
CC PRINTS: P00479; P00479.
CC PROSITE: P000384; PROKAR_ZN_DEPEND_PIRC; 1.
CC HYDROLASE; zinc; signal; Zymogen; Hemolysis; 3D-structure.
CC SIGNAL 1 24
CC PROPEP 25 38
CC CHAIN 39 283
CC METAL 32 52
CC METAL 52 52
CC METAL 93 93
CC METAL 107 107
CC METAL 156 156
CC METAL 160 160
CC METAL 166 166
CC METAL 180 180
CC METAL 184 184
CC METAL 184 184
CC VARIANT 212 212
CC VARIANT 226 226
CC VARIANT 239 239
CC VARIANT 282 282
CC SEQUENCE 283 AA; 32383 MW; AC3452FEF2E2B19 CRC64;

Query Match 48.8%; Score 39; DB 1; Length 283;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKMEATYP 9
DB 248 DKMEATYP 256

RESULT 9
PHLD_BACCE STANDARD: PRT: 283 AA.
AC P3376;1984 (Rel. 28, Created)
DT 01-SEP-1984 (Rel. 28, Last annotation update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE PHOSPHOLIPASE C PRECURSOR (EC 3.1.4.3) (PLC) (PHOSPHATIDYLCHOLINE
DE CHOLINEPHOSPHOHYDROLASE) (CERBOXYLASE) (A).
GN CEREA.
OS Bacillus cereus.
CC Bacillus, Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus.
CC NCBI:taxid:1986.
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-GP-4;
RA MEDLINE-69123149; PubMed-2536680;
RA Gilmore M.S., Cruz-Rodriguez A.L., Laineister-Waechecker M., Krefz J.,
RA Goebel M., "The cereus cytolytic determinant, cereolysin AB, which
RT complements the phospholipase C and sphingomyelinase genes: nucleotide
RT sequence and genetic linkage.",
RL J. Bacteriol. 171:744-753(1989).
RN 121
RP SEQUENCE OF 50-142 FROM N.A.
RA Gilmore M.S., Gilmore K.S., Goebel M.,
RA "A new strategy for ordered DNA sequencing based on a novel method for

```

```

RT the rapid purification of near-milligram quantities of a cloned
RT restriction fragment.",
RL Gene Anal. Tech. 2:108-114(1985).
CC 1- FUNCTION: REQUIRED. WITH SPHINGOMYELINASE TO EFFECT TARGET CELL
CC 1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O -> 1,2-
CC 1- DIACYLGLYCEROL + CHOLINE PHOSPHATE.
CC 1- COFACTOR: THREE ZINC IONS.
CC 1- SUBUNIT: MONOMER.
CC 1- SIMILARITY: TO BETA-HEMOLYSIN OF STAPHYLOCOCCUS AUREUS.
CC -----
CC THIS SWISS-PROT entry is supplied by a collaboration between the
CC European Bioinformatics Institute and the EMBL Outstation -
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.lsb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
CC EMBL: M2416: AAA91819.1
CC EMBL: M35411: AAA22524.1
CC PIR: A32042; A32042.
CC HSSP: P09598; IAH7.
CC InterPro: IPR001531;
CC Pfam: PF00882; ZN_dep_PIRC; 1.
CC PRINTS: P000384; PROKAR_ZN_DEPEND_PIRC; 1.
CC PROSITE: P000384; PROKAR_ZN_DEPEND_PIRC; 1.
CC HYDROLASE; zinc; signal; Zymogen; Hemolysis.
CC SIGNAL 1 24
CC PROPEP 25 38
CC CHAIN 39 283
CC METAL 32 52
CC METAL 52 52
CC METAL 93 93
CC METAL 107 107
CC METAL 156 156
CC METAL 160 160
CC METAL 166 166
CC METAL 180 180
CC METAL 184 184
CC SEQUENCE 283 AA; 32373 MW; 24D2E733402A644 CRC64;

Query Match 48.8%; Score 39; DB 1; Length 283;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DKMEATYP 9
DB 248 DKMEATYP 256

RESULT 10
VPL_BPCHP STANDARD: PRT: 595 AA.
AC P19192;1980 (Rel. 16, Created)
DT 01-NOV-1980 (Rel. 16, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROTEIN VPI (ORF1).
OS Bacteriophage Chpl.
CC Viruses.
CC NCBI:taxid:12367;
RN 1
RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-20.
RA MEDLINE-60111776; PubMed-2607341;
RA Storey C.C., Lusher M., Richmond S.J.;
RA "Analysis of the complete nucleotide sequence of Chpl1, a phage which
RT infects avian Chlamydia psittaci.",
RL J. Gen. Virol. 70:3981-3990(1989).
RN 2
RP THIS SWISS-PROT entry is supplied by a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.lsb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----

```

DR PRINTS: P800984; TRNA:SYNTHIF.
DR PROSITE: P800178; AL TRNA-LIGASE I; 1
KW Anticodon tRNA synthetases: Protein biosynthesis; LIGase; ATP-binding;
KW Metal-binding: Zinc.
FT SITE 53 63 *HIGH* REGION.
FT SITE 619 623 *KMSK* REGION.
FT BINDING 622 622 ATP (BY SIMILARITY).
SQ SOURCE: 1041 Mm; 117239 Mm; B5032828t8E08C6 CMC34;

Query Match 48.8%; Score 39; DB 1; Length 1041;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKENAVT 8
Db 134 DEMQAVT 141

RESULT 12
ID RPKX_SCHPO STANDARD: PRT: 71 AA.
DC 15-3077; 9034456; 36 Created)
DT 15-3077; 9034456; 36
DT 15-OCT-1998 (Rel. 35 (Created)
DT 15-OCT-2000 (Rel. 40, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE I, II, AND III B.3 KDA POLYPEPTIDE
DE (Pc 2.7.7.6) (AMC10-BETA).
DE RPB10 OR SPAC183.12C.
OS Schizosaccharomyces pombe (fission yeast).
OS Eukaryota; Eukaryota; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetes; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_Taxid=4896;
RN 11
RP SEQUENCE FROM N.A.
RP STRAIN-972;
RX MODLINE-97117445; PubMed=9054344;
RX POKRASKI G. V., Lebedenko E. N.,
RX "Phylogenetic relationships of nuclear RNA polymerases are
RX strictly conserved in all eukaryotes (letter)".
RX Bioorg. Khim. 22:938-940(1996).
RL 12
RL SEQUENCE FROM N.A.
RL STRAIN-972;
RL MODLINE-96271918; PubMed=9608944;
RL *Exon-intron organization of the gene encoding of
RL Schizosaccharomycetes pombe, coding for mini-subunits of nuclear RNA-
RL polymerase I-TII".
RL Mol. Biol. (Mosk) 32:285-290(1998).
RL 13
RL SEQUENCE FROM N.A.
RL STRAIN-972;
RL HARRIS D., BARNELL B.G., RAJAGOPALAN M.A., MOOD V.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBS
RL -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
RL OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
RL SUBSTRATES.
RL -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
RL (NMAR) - EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 15
RL DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS SHARED BY ALL 3 YEAST RNA
RL POLYMERASES
RL -1- SUBCELLULAR LOCATION: NUCLEAR
RL -1- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
RL FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
RL PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
RL III FOR 5S AND 5.8S GENES.
RL -1- SIMILAR MOLECULES: THE ARCHAEABACTERIA RPN0 / EUKARYOTIC RPB10
RL RNA POLYMERASE SUBUNIT FAMILY.
RL 14
RL THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration

Search completed: November 19, 2001, 08:25:35
Job time: 723 sec

```

05 Arabidopsis thaliana (Mouse-ear cress).
06 Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
07 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
08 Cnidaria; Antharia; Ascomycota; Basidiomycota; Charophyta;
09 NCH_TaxId=3702;
10
11 RP SEQUENCE FROM N.A.
12
13 RC STRAIN-CV. COLUMBIA;
14 MEDLINE=20083487; PubMed=10617197;
15 Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
16 Bujl C.B., Mason T.M., Bowman C.L., Barnstead M.E., Feldguy T.V.,
17 Holt C.B., Krasnoff S., Kunkin C.M., Kuo R., Moffat K.S.,
18 Cronin L.A., Shen W., Venter A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
19 Adams M.D., Carrara A.J., Fraser C.M., Venter J.C.;
20 Salzberg S.L., Fraser C.M., Venter J.C.;
21 "Sequence and analysis of chromosome 2 of the plant Arabidopsis
22 thaliana";
23 Nature 402:761-768(1999).
24
25 RN [2]
26
27 RP SEQUENCE OF 5-257 FROM N.A.
28 MEDLINE=94326944; PubMed=8050590;
29 Hartmann E., Prehn S.;
30
31 RA "The N-terminal region of the alpha-subunit of the TRAP complex has a
32 conserved cluster of negative charges.";
33 PUBMED=19325328(1994).
34
35 FT EES FUNCTION: 19325328(1994).
36
37 CC "1. BIND CA(2+) TO THE ER MEMBRANE AND THEREBY PROMOTE THE DEPOSITION
38 OF ER RESIDENT PROTEINS. MAY BE INVOLVED IN THE RECYCLING OF THE
39 TRANSLLOCATION APPARATUS AFTER COMPLETION OF THE TRANSLLOCATION
40 PROCESS OR MAY FUNCTION AS A MEMBRANE-BOUND CHAPERONE FACILITATING
41 FOLDING OF TRANSLOCATED PROTEINS.
42
43 -1- TRAP-GAMMA, HEPTOTETRAMER OF TRAP-ALPHA, TRAP-BETA, TRAP-DELTA AND
44 TRAP-EPSILON.
45
46 -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ENDOPLASMIC
47 RETICULUM.
48
49 CC -1- DOMAIN: SHOWS A REMARKABLE CHARGE DISTRIBUTION WITH THE N-TERMINUS
50 BEING HIGHLY NEGATIVELY CHARGED. AND THE CYTOPLASMIC C-TERMINUS
51 POSITIVELY CHARGED.
52
53 CC -1- PROSITE: POSITIVELY CHARGED IN ITS CYTOPLASMIC TAIL (BY SIMILARITY).
54
55 CC -1- MISCELLANEOUS: 19325328(1994).
56
57 CC "THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
58 BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
59 THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
60 USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
61 MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
62 PURPOSES WITHOUT A LICENSE AGREEMENT (SEE http://www.isb-sib.ch/announce/
63 OR SEND AN EMAIL TO license@sib.ch)".
64
65 CC -----
66 DR EMBL: AC006284; AAC29800.1;
67
68 DR EMBL: L32016; AAC21820.1;
69
70 KW Glycoprotein; Signal; Phosphorylation; Endoplasmic reticulum;
71 Transmembrane; Calcium-binding.
72
73 FT CHAIN 24 257
74
75 FT SUBUNIT
76
77 FT DOMAIN 24 189
78
79 FT TRANSSEM 190 208
80
81 FT DOMAIN 209 257
82
83 FT CARBOHYD 35 56
84
85 FT CARBOHYD 135 148
86
87 FT CARBOHYD 135 148
88
89 FT CARBOHYD 135 148
90
91 SEQUENCE 257 AA; 28036 MW; C43EDCA6B0D2653 CRC64;
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

```

Query Match

47.5%; Score 38; DB 1; Length 257;

Best Local Similarity 66.7%; Pred. No. 24;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 YITGADV 14

DB 146 YIOPGADV 154

THIS PAGE BLANK (USPTO)


```

ID 02KRY04 PRELIMINARY: PRT: 669 AA.
DC 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
GN PUTATIVE ALPHA-AMYLASE.
OS pepB.
OC Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Streptomycesaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=3503.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2)?;
RA Seeger K.J., Harris D.;
RT Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2)?;
RA Thomson N.R.;
RT Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2)?;
RA MEDLINE=97000351, PubMed=8843436;
RC STRAIN-A3(2)?;
RA Kinsahl H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: A1356932; CAB92881.1; -.
DR InterPro: IPR000533; -.
DR TrEMBL: P00019; ACTININ.1; UNKNOWN.1;
DR PROSITE: PS00430; TOMB_DEPENDENT_PRO_1; UNKNOWN.1.
SO SEQUENCE 669 AA: 74143 MW: 54630134C65518 CnC64;

Query Match 55.0%; Score 44; DB 2; Length 669;
Best Local Similarity 63.0%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DKWEATTPCA 11
DB 77 DKWATVTPCA 87

RESULT 8
ID 043395 PRELIMINARY: PRT: 682 AA.
AC 043395;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
GN P33-76 ASSOCIATED RNA SPLICING FACTOR.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97472464, PubMed=9328476;
RA Wang A., Foreman-Kay J., Luo Y., Luo M., Chow Y.H., Plumb J.;
RA Plesken J.D., Tsai L.C., Hong H.H., Woolford J.L., Jr., Hu J.;
RT "Identification and characterization of human genes encoding Hpr3p
RT and Hpr4p, interacting components of the spliceosome.";
RL Hum. Mol. Genet. 6:2117-2126(1997).
DR EMBL: AF001960; AAC09069.1; -.
DR TrEMBL: P01480; PWT.1;
DR SMART: SM00311; PWT.1;
DR InterPro: IPR000523; -.
SO SEQUENCE 682 AA: 77403 MW: 544608F72P39BA3 CnC64;

```

```

QY 3 WEATTPGAPD 14
DB 390 WDSYIIPGFDL 401

Query Match 55.0%; Score 44; DB 4; Length 682;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 WEATTPGAPD 14
DB 390 WDSYIIPGFDL 401

RESULT 9
ID 043446 PRELIMINARY: PRT: 683 AA.
AC 043446;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE 04/06 SMALL NUCLEAR RIBONUCLEOPROTEIN HPR3.
GN HPR3.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98067393, PubMed=9404889;
RA Hrovat D.S., Kobayashi R., Kralinger A.R.;
RT "The HPR3 protein is a homolog of the 100 kDa ribonucleoprotein
RT form a complex associated with U4/U5 snRNAs.";
RL RNA 3:1374-1387(1997).
DR EMBL: AF016370; AAC51926.1; -.
DR InterPro: IPR002483; -.
DR SMART: P01480; PWT.1;
DR TrEMBL: P01480; PWT.1;
DR PROSITE: PS00311; PWT.1;
DR InterPro: IPR000523; -.
SO SEQUENCE 683 AA: 77528 MW: 4A66AAC93110284 CnC64;

Query Match 55.0%; Score 44; DB 4; Length 683;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 WEATTPGAPD 14
DB 390 WDSYIIPGFDL 401

RESULT 10
ID 043449 PRELIMINARY: PRT: 333 AA.
AC 043449;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
GN UROKHO-PHYNOXEN DECARBOXYLASE RELATED PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9817288, PubMed=11029001;
RA Huppi H., Grail R., Stoeckli-Wasem M., Korotki K.K., Volter C.;
RA Mees H.-W., Frishman D., Stocker S., Lups A.N., Bannister K.;
RT "The genome sequence of the thermophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL: AA445063; CAC11495.1; -.
DR TrEMBL: IPR000257; -.
DR SMART: SM00311; PWT.1;
DR InterPro: IPR000523; -.
SO SEQUENCE 333 AA: 77528 MW: 4A66AAC93110284 CnC64;

```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:12:34 : Search time 77.92 Seconds
(without alignments)
10,892 Million cell updates/sec

Title: US-09-610-118-63

Sequence: 1 DKWEATITPCAFDV 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 41676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 41676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Minimum Match 1009
Listing first 45 summaries

Database :

A. Geneseq_0601:*

- 1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	80	100.0	14	AA61295	Anti-TMCO 268 scf
2	79	100.0	14	AA61295	Anti-TMCO 268 scf
3	44	53.8	207	AA634190	Zee may's protein f
4	43	53.8	217	AA634188	Zee may's protein f
5	43	53.8	223	AA634189	Zee may's protein f
6	41	51.2	312	AA818153	Plasmodium falciapa
7	41	51.2	363	AA818153	Soybean alpha-D-ga
8	41	51.2	378	AA818153	Alpha-galactosidase
9	41	51.2	378	AA818153	Alpha-galactosidase
10	41	51.2	378	AA818153	Alpha-galactosidase
11	41	51.2	410	AA818153	Alpha-galactosidase
12	41	51.2	410	AA818153	Alpha-galactosidase

12	41	51.2	420	16	AA81236	Coffee bean alpha-
13	41	51.2	420	16	AA81236	Heavy chain variab
14	40	50.0	117	15	AA852065	Heavy chain variab
15	40	50.0	117	15	AA852067	A human regulator
16	40	50.0	221	21	AA818667	Arabidopsis thalia
17	40	50.0	365	21	AA820888	Arabidopsis thalia
18	40	50.0	367	21	AA820887	Streptococcus pyog
19	40	50.0	366	21	AA820886	Streptococcus pyog
20	39	48.8	141	21	AA817040	Streptococcus pyog
21	39	48.8	155	21	AA817041	Streptococcus pyog
22	39	48.8	167	21	AA817046	Streptococcus pyog
23	39	48.8	167	21	AA817046	Streptococcus pyog
24	39	48.8	184	18	AA855630	H. pylori ORF 02ae
25	39	48.8	184	18	AA855630	H. pylori ORF 02ae
26	39	48.8	184	21	AA817039	Streptococcus pyog
27	39	48.8	217	21	AA817042	Streptococcus pyog
28	39	48.8	221	21	AA817045	Streptococcus pyog
29	39	48.8	221	21	AA817045	Streptococcus pyog
30	39	48.8	1045	13	AA857448	M. tuberculosis is
31	38	47.5	114	21	AA851263	Monoclonal antibody
32	38	47.5	117	11	AA804381	Variable heavy cha
33	38	47.5	117	11	AA804381	Sequence of VH-21P
34	38	47.5	117	20	AA857175	Human VH alpha2a
35	38	47.5	117	20	AA850683	Human VH alpha2a
36	38	47.5	117	21	AA857044	Human VH alpha2a
37	38	47.5	133	10	AA850884	Predicted sequence
38	38	47.5	133	11	AA804384	Colon Cancer monoc
39	38	47.5	133	14	AA838313	Sequence of murine
40	38	47.5	133	20	AA857177	Amino acid sequenc
41	38	47.5	133	20	AA857177	Human CCR3 protein
42	38	47.5	133	21	AA850716	CCR3 VH region pro
43	38	47.5	133	21	AA850716	CCR3 VH region pro
44	38	47.5	133	21	AA850716	Amino acid sequenc
45	38	47.5	133	21	AA850716	Amino acid sequenc

ALIGNMENTS

RESULT 1	AA61295	standard: Peptide: 14 AA.
1	AA61295	standard: Peptide: 14 AA.
AC	AA61295:	
XX		
DT	04-APR-2001 (first entry)	
DE	Anti-TMCO 268 scf CDR, SEQ ID NO: 63.	
XX		
KM	Human: antibody; scfv; CDR; complementarity determining region;	
KM	TMCO 268; cardiant; cerebroprotective; cytosolic; anticonvulsant;	
KM	thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;	
KM	platelet membrane glycoprotein receptor; bleeding disorder;	
KM	ischemic injury; thrombotic disorder; haemorrhagic disorder; stroke;	
KM	ischemia; cardiovascular disease; immunological disease; liver disorder;	
XX	cancer.	
OS	Homo sapiens.	
XX		
PN	WO200100810-A1.	
PD	04-JUN-2001.	
XX		
PR	30-JUN-2000; 2000MO-US18152.	
XX		
PR	30-JUN-1999; 99US-0345468-	
PR	06-DEC-1999; 99US-0454824-	
PR	14-FEB-2000; 2000US-050387.	
XX		
PR	(MILL-) MILLENNIUM PHARM INC.	
PI	Buflerf SJ, Willelaj J, Jandrot-Perrus M, Valinchenker W, Gilli DS, Qian MD, Kingsbury G;	

[illegible]

PR	23	-JUL-1999	9905-014514.15	PR	23	-JUL-1999	9905-014514.15
PR	23	-JUL-1999	9905-014522.18	PR	23	-JUL-1999	9905-014522.18
PR	23	-JUL-1999	9905-014524.24	PR	23	-JUL-1999	9905-014524.24
PR	25	-JUL-1999	9905-014526.95	PR	25	-JUL-1999	9905-014526.95
PR	27	-JUL-1999	9905-014531.18	PR	27	-JUL-1999	9905-014531.18
PR	27	-JUL-1999	9905-014531.18	PR	27	-JUL-1999	9905-014531.18
PR	28	-JUL-1999	9905-014535.11	PR	28	-JUL-1999	9905-014535.11
PR	02	-AUG-1999	9905-014538.66	PR	02	-AUG-1999	9905-014538.66
PR	02	-AUG-1999	9905-014538.68	PR	02	-AUG-1999	9905-014538.68
PR	03	-AUG-1999	9905-014540.38	PR	03	-AUG-1999	9905-014540.38
PR	03	-AUG-1999	9905-014540.38	PR	03	-AUG-1999	9905-014540.38
PR	03	-AUG-1999	9905-014540.38	PR	03	-AUG-1999	9905-014540.38
PR	03	-AUG-1999	9905-014540.38	PR	03	-AUG-1999	9905-014540.38
PR	03	-AUG-1999	9905-014540.38	PR	03	-AUG-1999	9905-014540.38
PR	06	-AUG-1999	9905-014716.01	PR	06	-AUG-1999	9905-014716.01
PR	06	-AUG-1999	9905-014716.01	PR	06	-AUG-1999	9905-014716.01
PR	09	-AUG-1999	9905-014743.93	PR	09	-AUG-1999	9905-014743.93
PR	09	-AUG-1999	9905-014743.93	PR	09	-AUG-1999	9905-014743.93
PR	09	-AUG-1999	9905-014743.93	PR	09	-AUG-1999	9905-014743.93
PR	10	-AUG-1999	9905-014743.93	PR	10	-AUG-1999	9905-014743.93
PR	12	-AUG-1999	9905-014834.41	PR	12	-AUG-1999	9905-014834.41
PR	13	-AUG-1999	9905-014856.65	PR	13	-AUG-1999	9905-014856.65
PR	13	-AUG-1999	9905-014868.84	PR	13	-AUG-1999	9905-014868.84
PR	17	-AUG-1999	9905-014917.75	PR	17	-AUG-1999	9905-014917.75
PR	18	-AUG-1999	9905-014942.28	PR	18	-AUG-1999	9905-014942.28
PR	18	-AUG-1999	9905-014942.28	PR	18	-AUG-1999	9905-014942.28
PR	18	-AUG-1999	9905-014942.28	PR	18	-AUG-1999	9905-014942.28
PR	20	-AUG-1999	9905-014962.20	PR	20	-AUG-1999	9905-014962.20
PR	20	-AUG-1999	9905-014962.20	PR	20	-AUG-1999	9905-014962.20
PR	23	-AUG-1999	9905-015056.93	PR	23	-AUG-1999	9905-015056.93
PR	25	-AUG-1999	9905-015069.30	PR	25	-AUG-1999	9905-015069.30
PR	26	-AUG-1999	9905-015108.04	PR	26	-AUG-1999	9905-015108.04
PR	27	-AUG-1999	9905-015108.04	PR	27	-AUG-1999	9905-015108.04
PR	27	-AUG-1999	9905-015108.04	PR	27	-AUG-1999	9905-015108.04
PR	30	-AUG-1999	9905-015130.03	PR	30	-AUG-1999	9905-015130.03
PR	31	-AUG-1999	9905-015130.03	PR	31	-AUG-1999	9905-015130.03
PR	01	-SEP-1999	9905-015139.38	PR	01	-SEP-1999	9905-015139.38
PR	01	-SEP-1999	9905-015139.38	PR	01	-SEP-1999	9905-015139.38
PR	07	-SEP-1999	9905-015307.65	PR	07	-SEP-1999	9905-015307.65
PR	10	-SEP-1999	9905-015327.58	PR	10	-SEP-1999	9905-015327.58
PR	11	-SEP-1999	9905-015327.58	PR	11	-SEP-1999	9905-015327.58
PR	15	-SEP-1999	9905-015403.33	PR	15	-SEP-1999	9905-015403.33
PR	20	-SEP-1999	9905-015477.99	PR	20	-SEP-1999	9905-015477.99
PR	22	-SEP-1999	9905-015513.39	PR	22	-SEP-1999	9905-015513.39
PR	23	-SEP-1999	9905-015513.39	PR	23	-SEP-	

PR 28-OCT-1999: 9905-0145951.
 PR 02-AUG-1999: 9905-0146386.
 PR 02-OCT-1999: 9905-0146387.
 PR 02-AUG-1999: 9905-0146388.
 PR 03-AUG-1999: 9905-0147038.
 PR 04-AUG-1999: 9905-0147204.
 PR 04-AUG-1999: 9905-0147302.
 PR 05-AUG-1999: 9905-0147192.
 PR 06-AUG-1999: 9905-0147260.
 PR 06-AUG-1999: 9905-0147303.
 PR 09-AUG-1999: 9905-0147443.
 PR 09-AUG-1999: 9905-0147935.
 PR 10-AUG-1999: 9905-0148171.
 PR 11-AUG-1999: 9905-0148319.
 PR 12-AUG-1999: 9905-0148341.
 PR 13-AUG-1999: 9905-0148565.
 PR 13-AUG-1999: 9905-0148684.
 PR 17-AUG-1999: 9905-0148175.
 PR 18-AUG-1999: 9905-0149426.
 PR 20-AUG-1999: 9905-0149722.
 PR 20-AUG-1999: 9905-0149723.
 PR 20-AUG-1999: 9905-0149929.
 PR 23-AUG-1999: 9905-0149902.
 PR 23-AUG-1999: 9905-0149970.
 PR 25-AUG-1999: 9905-0150584.
 PR 25-AUG-1999: 9905-0150884.
 PR 27-AUG-1999: 9905-0151065.
 PR 27-AUG-1999: 9905-0151066.
 PR 27-AUG-1999: 9905-0151080.
 PR 30-AUG-1999: 9905-0151303.
 PR 31-AUG-1999: 9905-0151438.
 PR 31-AUG-1999: 9905-0151513.
 PR 07-SEP-1999: 9905-0152353.
 PR 10-SEP-1999: 9905-0153070.
 PR 13-SEP-1999: 9905-0153758.
 PR 15-SEP-1999: 9905-0154018.
 PR 16-SEP-1999: 9905-0154039.
 PR 20-SEP-1999: 9905-0154779.
 PR 22-SEP-1999: 9905-0155139.
 PR 23-SEP-1999: 9905-0155179.
 PR 24-SEP-1999: 9905-0155659.
 PR 28-SEP-1999: 9905-0156458.
 PR 29-SEP-1999: 9905-0156599.
 PR 04-OCT-1999: 9905-0157117.
 PR 05-OCT-1999: 9905-0157753.
 PR 06-OCT-1999: 9905-0157865.
 PR 07-OCT-1999: 9905-0158079.
 PR 10-OCT-1999: 9905-0158169.
 PR 12-OCT-1999: 9905-0159293.
 PR 13-OCT-1999: 9905-0159294.
 PR 13-OCT-1999: 9905-0159295.
 PR 14-OCT-1999: 9905-0159329.
 PR 14-OCT-1999: 9905-0159350.
 PR 14-OCT-1999: 9905-0159371.
 PR 14-OCT-1999: 9905-0159568.
 PR 18-OCT-1999: 9905-0159584.
 PR 21-OCT-1999: 9905-0160741.
 PR 21-OCT-1999: 9905-0160767.
 PR 21-OCT-1999: 9905-0160768.
 PR 21-OCT-1999: 9905-0160770.
 PR 21-OCT-1999: 9905-0160814.
 PR 21-OCT-1999: 9905-0160815.
 PR 22-OCT-1999: 9905-0160980.
 PR 22-OCT-1999: 9905-0160981.
 PR 22-OCT-1999: 9905-0160989.
 PR 25-OCT-1999: 9905-0161404.
 PR 25-OCT-1999: 9905-0161405.
 PR 25-OCT-1999: 9905-0161406.
 PR 26-OCT-1999: 9905-0161599.

PR 26-OCT-1999: 9905-0161360.
 PR 26-OCT-1999: 9905-0161361.
 PR 26-OCT-1999: 9905-0161392.
 PR 28-OCT-1999: 9905-0161992.
 PR 28-OCT-1999: 9905-0161993.
 PR 29-OCT-1999: 9905-0162142.

 Query Match 53.8%; Score 43; DB 21; Length 217;
 Best Local Similarity 42.9%; Pred. No. 8.7;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DKEATTPGADVD 14
 Db 93 eweallptgdnf 106

 RESULT 5
 AAC34188 standard; Protein: 223 AA.
 XX
 AC AAC34188:
 XX
 DT 18-OCT-2000 (first entry)
 XX
 DE Zoa mays protein fragment SEQ ID NO: 41559.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 hybridisation assay; genetic mapping; gene expression control; promoter;
 termination sequence; corn.
 XX
 OS Zoa mays subsp. mays.
 XX
 XX
 XX EPI03405-A2.
 PD 06-SEP-2000.
 XX
 PE 25-FEB-2000: 2000EP-0301439.
 XX
 PR 25-FEB-1999: 9905-0121825.
 PR 05-MAR-1999: 9905-0122150.
 PR 23-MAR-1999: 9905-0123788.
 PR 25-MAR-1999: 9905-0125284.
 PR 29-MAR-1999: 9905-0126785.
 PR 01-APR-1999: 9905-0127462.
 PR 06-APR-1999: 9905-0128234.
 PR 18-APR-1999: 9905-0128714.
 PR 19-APR-1999: 9905-0128655.
 PR 23-APR-1999: 9905-0130449.
 PR 23-APR-1999: 9905-0130510.
 PR 23-APR-1999: 9905-0130891.
 PR 28-APR-1999: 9905-0131449.
 PR 30-APR-1999: 9905-0132048.
 PR 30-APR-1999: 9905-0132407.
 PR 04-MAY-1999: 9905-0132454.
 PR 05-MAY-1999: 9905-0132471.
 PR 06-MAY-1999: 9905-0132486.
 PR 07-MAY-1999: 9905-0132487.
 PR 07-MAY-1999: 9905-0132683.
 PR 11-MAY-1999: 9905-0134256.
 PR 14-MAY-1999: 9905-0134218.
 PR 14-MAY-1999: 9905-0134219.
 PR 14-MAY-1999: 9905-0134271.
 PR 14-MAY-1999: 9905-0134272.
 PR 16-MAY-1999: 9905-0134788.
 PR 19-MAY-1999: 9905-0134941.
 PR 20-MAY-1999: 9905-0135134.
 PR 21-MAY-1999: 9905-0135333.
 PR 24-MAY-1999: 9905-0135629.
 PR 25-MAY-1999: 9905-0136071.
 PR 27-MAY-1999: 9905-0136282.
 PR 28-MAY-1999: 9905-0136782.

PR 01-JUN-1999: 9905-0137222.
PR 03-JUN-1999: 9905-0137558.
PR 04-JUN-1999: 9905-0137502.
PR 05-JUN-1999: 9905-0137604.
PR 06-JUN-1999: 9905-0137674.
PR 10-JUN-1999: 9905-0138547.
PR 10-JUN-1999: 9905-0138847.
PR 14-JUN-1999: 9905-0139119.
PR 16-JUN-1999: 9905-0139452.
PR 16-JUN-1999: 9905-0139453.
PR 16-JUN-1999: 9905-0139454.
PR 16-JUN-1999: 9905-0139455.
PR 18-JUN-1999: 9905-0139456.
PR 18-JUN-1999: 9905-0139457.
PR 18-JUN-1999: 9905-0139458.
PR 18-JUN-1999: 9905-0139459.
PR 18-JUN-1999: 9905-0139460.
PR 18-JUN-1999: 9905-0139461.
PR 18-JUN-1999: 9905-0139463.
PR 18-JUN-1999: 9905-0139750.
PR 18-JUN-1999: 9905-0139763.
PR 21-JUN-1999: 9905-0139817.
PR 22-JUN-1999: 9905-0139899.
PR 22-JUN-1999: 9905-0140353.
PR 23-JUN-1999: 9905-0140655.
PR 24-JUN-1999: 9905-0140683.
PR 28-JUN-1999: 9905-0140823.
PR 29-JUN-1999: 9905-0140991.
PR 30-JUN-1999: 9905-0141287.
PR 01-JUL-1999: 9905-0141842.
PR 02-JUL-1999: 9905-0142154.
PR 02-JUL-1999: 9905-0142390.
PR 06-JUL-1999: 9905-0142803.
PR 09-JUL-1999: 9905-0142920.
PR 12-JUL-1999: 9905-0143977.
PR 13-JUL-1999: 9905-0143942.
PR 15-JUL-1999: 9905-0143654.
PR 15-JUL-1999: 9905-0144085.
PR 16-JUL-1999: 9905-0144086.
PR 16-JUL-1999: 9905-0144325.
PR 19-JUL-1999: 9905-0144331.
PR 19-JUL-1999: 9905-0144332.
PR 19-JUL-1999: 9905-0144333.
PR 19-JUL-1999: 9905-0144334.
PR 19-JUL-1999: 9905-0144352.
PR 20-JUL-1999: 9905-0144632.
PR 20-JUL-1999: 9905-0144684.
PR 21-JUL-1999: 9905-0144814.
PR 21-JUL-1999: 9905-0145086.
PR 21-JUL-1999: 9905-0145088.
PR 22-JUL-1999: 9905-0145089.
PR 22-JUL-1999: 9905-0145087.
PR 22-JUL-1999: 9905-0145192.
PR 22-JUL-1999: 9905-0145145.
PR 23-JUL-1999: 9905-0145218.
PR 23-JUL-1999: 9905-0145224.
PR 25-JUL-1999: 9905-0145216.
PR 27-JUL-1999: 9905-0145318.
PR 27-JUL-1999: 9905-0145919.
PR 28-JUL-1999: 9905-0145951.
PR 02-AUG-1999: 9905-0146386.
PR 02-AUG-1999: 9905-0146388.
PR 03-AUG-1999: 9905-0146389.
PR 04-AUG-1999: 9905-0147204.
PR 04-AUG-1999: 9905-0147302.

PR 05-AUG-1999: 9905-0147192.
PR 05-AUG-1999: 9905-0147260.
PR 06-AUG-1999: 9905-0147303.
PR 06-AUG-1999: 9905-0147416.
PR 09-AUG-1999: 9905-0147493.
PR 09-AUG-1999: 9905-0147935.
PR 11-AUG-1999: 9905-0148311.
PR 12-AUG-1999: 9905-0148341.
PR 13-AUG-1999: 9905-0148565.
PR 16-AUG-1999: 9905-0148664.
PR 16-AUG-1999: 9905-0149368.
PR 17-AUG-1999: 9905-0149175.
PR 20-AUG-1999: 9905-0149426.
PR 20-AUG-1999: 9905-0149723.
PR 20-AUG-1999: 9905-0149929.
PR 23-AUG-1999: 9905-0149922.
PR 23-AUG-1999: 9905-0149930.
PR 25-AUG-1999: 9905-0150566.
PR 25-AUG-1999: 9905-0150884.
PR 25-AUG-1999: 9905-0150882.
PR 27-AUG-1999: 9905-0151062.
PR 27-AUG-1999: 9905-0151080.
PR 30-AUG-1999: 9905-0151303.
PR 31-AUG-1999: 9905-0151438.
PR 01-SEP-1999: 9905-0151930.
PR 01-SEP-1999: 9905-0152353.
PR 01-SEP-1999: 9905-0152758.
PR 15-SEP-1999: 9905-0153758.
PR 16-SEP-1999: 9905-0154039.
PR 20-SEP-1999: 9905-0154779.
PR 22-SEP-1999: 9905-0155139.
PR 23-SEP-1999: 9905-0155486.
PR 23-SEP-1999: 9905-0156459.
PR 28-SEP-1999: 9905-0156596.
PR 04-OCT-1999: 9905-0157117.
PR 05-OCT-1999: 9905-0157753.
PR 06-OCT-1999: 9905-0157655.
PR 07-OCT-1999: 9905-0158029.
PR 07-OCT-1999: 9905-0158422.
PR 12-OCT-1999: 9905-0158422.
PR 13-OCT-1999: 9905-0159293.
PR 13-OCT-1999: 9905-0159294.
PR 13-OCT-1999: 9905-0159295.
PR 14-OCT-1999: 9905-0159329.
PR 14-OCT-1999: 9905-0159330.
PR 14-OCT-1999: 9905-0159331.
PR 14-OCT-1999: 9905-0159584.
PR 18-OCT-1999: 9905-0159584.
PR 21-OCT-1999: 9905-0160741.
PR 21-OCT-1999: 9905-0160761.
PR 21-OCT-1999: 9905-0160768.
PR 21-OCT-1999: 9905-0160770.
PR 21-OCT-1999: 9905-0160814.
PR 21-OCT-1999: 9905-0160815.
PR 22-OCT-1999: 9905-0160980.
PR 22-OCT-1999: 9905-0160981.
PR 22-OCT-1999: 9905-0160989.
PR 25-OCT-1999: 9905-0161404.
PR 25-OCT-1999: 9905-0161405.
PR 25-OCT-1999: 9905-0161406.
PR 25-OCT-1999: 9905-0161407.
PR 26-OCT-1999: 9905-0161160.
PR 26-OCT-1999: 9905-0161261.
PR 26-OCT-1999: 9905-0161920.
PR 26-OCT-1999: 9905-0161922.
PR 26-OCT-1999: 9905-0161993.
PR 29-OCT-1999: 9905-0162142.

XX Alpha-galactosidase of green coffee bean.
 XX Alpha-galactosidase; coffee bean; CBG; alpha-1,3-linked galactose;
 XX B antigen; blood group; S19.
 XX Coffea sp.
 FH Key
 FH Peptide Location/Qualifiers
 FT 1..15
 FT /label= Sig-peptide
 XX MO9507088-A.
 XX 16-MAR-1995.
 XX 26-AUG-1994; 94MO-US09662.
 XX 08-SEP-1993; 93US-0118470.
 XX (NYBL-) NEW YORK BLOOD CENT INC.
 PA Goldstein J, Zhu A;
 PI WPI: 1995-123231/16.
 DR N-PSDB: AAO83523.
 XX Now recombinant coffee bean alpha-galactosidase - used for
 PT cleaving alpha1,3-linked galactose residues on the surface of
 PT cells for prodn. of blood prods.
 XX
 XX Disclosure: Page 38-39; 67pp; English.
 XX
 XX DNA encoding coffee bean alpha-galactosidase (CBG) was obtained by
 CC isolating mRNA from coffee beans, cDNA and subcloning this
 CC to PCR amplification using primers
 CC sequence of CBG. A full-length cDNA clone is given in AAO3353, which
 CC encoded a 42 kDa protein (AA070205). Recombinant CBG was produced in
 CC Sf9 cells.
 XX
 XX Sequence 378 AA:
 SO
 Query Match 51.2%; Score 41; DB 16; Length 378;
 Best Local Similarity 46.2%; Pred. No. 35;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 1 DKEXAYITPCARD 13
 ||| : : : : :
 DB 216 dkwaaygpgywn 228
 RESULT 9
 ID AAM00621 standard; Protein: 378 AA.
 AC AAM00621;
 XX 15-NOV-1996 (first entry)
 DT Coffee bean alpha-galactosidase.
 DE Alpha-galactosidase; coffee; blood group; B antigen;
 XX Pichia pastoris.
 XX
 OS Coffea sp.
 FH Key
 FH Peptide Location/Qualifiers
 FT 1..15
 FT /label= Sig-peptide
 FT Modified-site /label= N-linked-glycosylation-site
 FT /label= N-linked-glycosylation-site
 XX

PN MO9623869-A1.
 PD 08-AUG-1996.
 XX 30-JAN-1996; 96MO-US01212.
 PF 30-JAN-1995; 95US-0380194.
 XX (NYBL-) NEW YORK BLOOD CENT INC.
 PA Goldstein J, Zhu A;
 PI WPI: 1996-371420/37.
 DR N-PSDB: AAT35799.
 XX Now recombinant coffee bean alpha-galactosidase - used partic. for
 PT removing B antigens from the surface of cells in blood prods.
 XX
 XX Example 1: Fig 1A-B; 56pp; English.
 PS
 CC The amino acid sequence (AAM00621) of coffee bean full-length alpha-
 CC galactosidase was deduced from a cDNA clone (AAT93799) obt'd. from
 CC cDNA library of coffee bean. The recombinant enzyme
 CC was achieved using Pichia pastoris as host.
 CC to cleave galactose sugar residues, partic. alpha-1,3-linked
 CC galactose residues. It is useful for the removal of type B antigens
 CC from the surface of cells in blood prods., thereby converting type
 CC B blood prods. to type O, and type AB to type A without affecting
 CC the surface or function of the cells.
 XX
 XX Sequence 378 AA:
 SO

Query Match 51.2%; Score 41; DB 17; Length 378;
 Best Local Similarity 46.2%; Pred. No. 35;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 1 DKEXAYITPCARD 13
 ||| : : : : :
 DB 216 dkwaaygpgywn 228
 RESULT 10
 ID AAM26604 standard; Protein: 406 AA.
 AC AAM26604;
 XX 27-JAN-1998 (first entry)
 DT Senna alpha-galactosidase.
 DE Alpha-galactosidase; mannoside; galactose; galactomannan; guar gum;
 XX Locust bean gum; transgenic plant.
 XX
 OS Senna.
 FH Key
 FH Peptide Location/Qualifiers
 FT 12-JUN-1997.
 PD 02-DEC-1996; 96MO-EP05581.
 PF 04-DEC-1995; 95GB-0024752.
 XX (DANIT-) DANISCO AS.
 PA Brunstedt J, Jorboe M, Petersen SG;
 PI WPI: 1997-319783/29.
 DR N-PSDB: AAT90432.
 XX In vivo modification process that affects the mannoside-to-galactose

QY 1 DKRATITPGADV 13
111 : 11 : :
Db 258 dkasypgpgpym 270

RESULT 13

ID AAR52061 standard; Protein: 116 AA.

XX AAR52061:

DT 11-OCT-1996 (first entry)

DE Heavy chain variable region of murine anti-N901 antibody.

XX antibody: humanised; murine; human; heavy chain; light; variable;
XX framework region; complementarity determining region; reshaping;
XX modelling; surface residue; modify.

OS Mus sp.

XX Key

FT Region

FT /label=framework_region_1

FT /note=FR 1*

FT /label=framework_region_1

FT /note=CDR 1*

FT /note=FR 2*

FT /note=CDR 2*

FT /note=FR 3*

FT /note=CDR 3*

XX EP592106-A1.

XX 13-APR-1994.

XX 07-SEP-1993; 93EP-0307051.

XX 09-SEP-1992; 92US-0942245.

XX (PEDERSEN J T.

XX (IMMUNO-) IMMUNOGEN INC.

XX GULD BC, Pedersen JT, Rees AR, Roguska MA, Seattle SMJ;

XX WPI; 1994-120230/15.

XX Method of resurfacing of rodent antibodies to produce humanised
XX antibody forms - for producing non-human antibodies with improved
XX therapeutic efficiency by presenting human surface on V-region

XX Example 1: Fig 4B: 230pp; English.

XX Modification of a rodent antibody or fragment by resurfacing in order
XX to produce a humanised rodent antibody can be determined by calculating
XX homology between murine and human antibody surfaces. In order to test
XX the resurfacing approach of the invention, three humanisation experiments
XX were performed: (1) traditional loop grafting; (2) resurfacing approach
XX using most similar chain and (3) resurfacing approach using human
XX sequences with most similar surface residues. The antibody of human
XX chain variable region. Numbering of which the present sequence is the heavy
XX starts at 118.

XX Sequence 116 AA:

Query Match 50.0%; Score 40; DB 15; Length 116;

QY 2 KMRATITPGADV 14
111 : 11 : :
Db 46 dkaylssgscfl 58

RESULT 14

ID AAR52065 standard; Protein: 117 AA.

XX AAR52065:

DT 11-OCT-1996 (first entry)

DE Heavy chain variable region of humanised N901/036005 antibody.

XX antibody: humanised; murine; human; heavy chain; light; variable;
XX framework region; complementarity determining region; reshaping;
XX modelling; surface residue; modify.

OS Chimeric Homo sapiens.

XX Chimeric Mus sp.

XX Key

FT Region

FT /label=framework_region_1

FT /note=FR 1*

FT /label=framework_region_1

FT /note=CDR 1*

FT /note=FR 2*

FT /note=CDR 2*

FT /note=FR 3*

FT /note=CDR 3*

XX EP592106-A1.

XX 13-APR-1994.

XX 07-SEP-1993; 93EP-0307051.

XX 09-SEP-1992; 92US-0942245.

XX (PEDERSEN J T.

XX (IMMUNO-) IMMUNOGEN INC.

XX GULD BC, Pedersen JT, Rees AR, Roguska MA, Seattle SMJ;

XX WPI; 1994-120230/15.

XX Method of resurfacing of rodent antibodies to produce humanised
XX antibody forms - for producing non-human antibodies with improved
XX therapeutic efficiency by presenting human surface on V-region

XX Example 1: Fig 4B: 230pp; English.

XX Modification of a rodent antibody (Ab) or fragment by resurfacing in
XX order to produce a humanised rodent Ab can be determined by calculating
XX homology between murine and human Ab antibody surfaces. In order to test
XX the resurfacing approach of the invention, three humanisation experiments
XX were set up: (1) traditional loop grafting; (2) resurfacing approach
XX using most similar chain; and (3) resurfacing approach using human
XX sequences with most similar surface residues. The Ab used was the
XX murine anti-N901 Ab (see AAR52061). The AAG36005 Ab (AAR52065) which has
XX 89 percent homology with anti-N901 Ab was used in the resurfacing
XX approach using most similar chain and the present sequence.
XX N901/AAG36005, was produced with 103 percent homology to anti-N901 Ab.

```

XX      1
SQ      Sequence      117 AA:
Query Match      50.0%: Score 40; DB 15; Length 117:
Best Local Similarity 46.2%: Pred. No. 15:
Matches 6: Conservative 4; Mismatches 3; Indels 0; Gaps 0:
OY      2 KMEAYITPGAFDV 14
       : 1 1 1 1 1 1 :
DB      46 ewaylissgftl 58

RESULT 15
AAR52067
ID      AAR52067 standard; Protein: 117 AA.
AC      AAR52067;
XX
XX      11-OCT-1996 (first entry)
XX
DE      Heavy chain variable region of humanised N901/P10123 antibody.
XX
XX      antibody: humanised; murine; human; heavy chain; light: variable;
KM      framework region; complementarity determining region; reshaping;
KW      modelling; surface residue; modify.
XX
XX      Chimeric Homo sapiens.
OS      Chimeric Mus sp.
XX
XX      Key
FH      Region      Location/Qualifiers
FT      Region      1..30      //label=framework_region_1
FT      Region      31..58      //note=FR 1*
FT      Region      59..107 //label=complementarity_determining_region_1
FT      Region      108..135 //note=CDR 1*
FT      Region      136..163 //note=FR 2*
FT      Region      164..191 //note=CDR 2*
FT      Region      192..219 //note=FR 3*
FT      Region      220..247 //note=CDR 3*
XX
XX      EP592106-A1.
XX
XX      13-APR-1994.
XX
XX      07-SEP-1993; 93EP-0307051.
XX
XX      09-SEP-1992; 92US-094245.
XX
XX      (PEDE/) PEDERSEN J T.
XX      (IMMU-) IMMUNOGEN INC.
XX
XX      Gullid BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
XX      WPL: 1994-120230/15.
XX
XX      Method of resurfacing of rodent antibodies to produce humanised
XX      antibody forms - for producing non-human antibodies with improved
XX      therapeutic efficiency by presenting human surface on v-region
XX
XX      Example 1; Fig 4b; 230pp: English.
XX
XX      Modification of a rodent antibody (Ab) or fragment by resurfacing in
XX      order to produce a humanised rodent Ab can be determined by calculating
XX      homology between murine and human Ab antibody surfaces. In order to test
XX      the resurfacing approach of the invention, three humanisation
XX      experiments were set up: (1) traditional loop grafting; (2) resurfacing
XX      approach using most similar chain; and (3) resurfacing approach using

```

```

CC      human sequences with most similar surface residues. The Ab used was the
CC      murine anti-N901 Ab (see AAR52061). The P10123 Ab (AAR52067) which has 74
CC      percent homology with the murine Ab was used in the resurfacing approach
CC      to produce humanised Ab antibody surfaces and the present sequence
CC      N901/P10123, was produced with 110 percent homology to anti-N901 Ab.
CC      Sequence numbering starts at 118 in the specification.
XX
XX      SQ      Sequence      117 AA:

```

```

Query Match      50.0%: Score 40; DB 15; Length 117:
Best Local Similarity 46.2%: Pred. No. 15:
Matches 6: Conservative 4; Mismatches 3; Indels 0; Gaps 0:
OY      2 KMEAYITPGAFDV 14
       : 1 1 1 1 1 1 :
DB      46 ewaylissgftl 58

```

Search completed: November 19, 2001, 08:12:35
Job time: 88 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:23:14 ; Search time 526.89 Seconds
(without alignments)
7.378 Million cell updates/sec

Title: US-09-610-118-63

Perfect score: 80

Sequence: 1 DKWEAYITPCARDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277557034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Pending Patents, AA, Main *

1: /cgn2.6/p/cdata/2/paa/US06.COMB.pep.*
2: /cgn2.6/p/cdata/2/paa/US06.COMB.pep.*
3: /cgn2.6/p/cdata/2/paa/US07.COMB.pep.*
4: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
5: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
6: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
7: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
8: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
9: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
10: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
11: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
12: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
13: /cgn2.6/p/cdata/2/paa/US08.COMB.pep.*
14: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
15: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
16: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
17: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
18: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
19: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
20: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
21: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
22: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
23: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*
24: /cgn2.6/p/cdata/2/paa/US09.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	1	1	PCT-US00-18152-63	Sequence 63, Appl
2	100.0	14	20	US-09-610-118-63	Sequence 63, Appl
3	80	100.0	14	US-09-832-312-63	Sequence 63, Appl
4	47	58.8	111	US-09-213-103-10	Sequence 10, Appl
5	47	58.8	111	US-09-049-022-3	Sequence 3, Appl
6	47	58.8	325	PCT-US98-2042-9	Sequence 3, Appl
7	47	58.8	325	PCT-US98-3042-3	Sequence 3, Appl
8	47	58.8	325	US-09-150-857-10	Sequence 10, Appl
9	47	58.8	325	US-09-150-857-10	Sequence 10, Appl

10	47	58.8	325	15	US-09-150-857-10	Sequence 10, Appl
11 <td>47 <th>58.8</th> <td>325</td> <td>16 <td>US-09-213-103-5</td> <td>Sequence 5, Appl</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>16 <td>US-09-213-103-5</td> <td>Sequence 5, Appl</td> </td>	58.8	325	16 <td>US-09-213-103-5</td> <td>Sequence 5, Appl</td>	US-09-213-103-5	Sequence 5, Appl
12 <td>47 <th>58.8</th> <td>325</td> <td>16 <td>US-09-213-164-5</td> <td>Sequence 5, Appl</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>16 <td>US-09-213-164-5</td> <td>Sequence 5, Appl</td> </td>	58.8	325	16 <td>US-09-213-164-5</td> <td>Sequence 5, Appl</td>	US-09-213-164-5	Sequence 5, Appl
13 <td>47 <th>58.8</th> <td>325</td> <td>16 <td>US-09-284-320-50</td> <td>Sequence 90, Appl</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>16 <td>US-09-284-320-50</td> <td>Sequence 90, Appl</td> </td>	58.8	325	16 <td>US-09-284-320-50</td> <td>Sequence 90, Appl</td>	US-09-284-320-50	Sequence 90, Appl
14 <td>47 <th>58.8</th> <td>325</td> <td>16 <td>US-09-292-228-10</td> <td>Sequence 10, Appl</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>16 <td>US-09-292-228-10</td> <td>Sequence 10, Appl</td> </td>	58.8	325	16 <td>US-09-292-228-10</td> <td>Sequence 10, Appl</td>	US-09-292-228-10	Sequence 10, Appl
15 <td>47 <th>58.8</th> <td>325</td> <td>21 <td>US-09-717-778-9</td> <td>Sequence 9, Appl</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>21 <td>US-09-717-778-9</td> <td>Sequence 9, Appl</td> </td>	58.8	325	21 <td>US-09-717-778-9</td> <td>Sequence 9, Appl</td>	US-09-717-778-9	Sequence 9, Appl
16 <td>47 <th>58.8</th> <td>325</td> <td>21 <td>US-09-739-451-5</td> <td>Sequence 5, Appl</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>21 <td>US-09-739-451-5</td> <td>Sequence 5, Appl</td> </td>	58.8	325	21 <td>US-09-739-451-5</td> <td>Sequence 5, Appl</td>	US-09-739-451-5	Sequence 5, Appl
17 <td>47 <th>58.8</th> <td>325</td> <td>22 <td>US-08-904-006-10</td> <td>Sequence 10, Appl</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>22 <td>US-08-904-006-10</td> <td>Sequence 10, Appl</td> </td>	58.8	325	22 <td>US-08-904-006-10</td> <td>Sequence 10, Appl</td>	US-08-904-006-10	Sequence 10, Appl
18 <td>47 <th>58.8</th> <td>325</td> <td>22 <td>US-08-904-322-2114</td> <td>Sequence 2114, Appl</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>22 <td>US-08-904-322-2114</td> <td>Sequence 2114, Appl</td> </td>	58.8	325	22 <td>US-08-904-322-2114</td> <td>Sequence 2114, Appl</td>	US-08-904-322-2114	Sequence 2114, Appl
19 <td>47 <th>58.8</th> <td>325</td> <td>24 <td>US-60-167-167-10119</td> <td>Sequence 10119, A</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>24 <td>US-60-167-167-10119</td> <td>Sequence 10119, A</td> </td>	58.8	325	24 <td>US-60-167-167-10119</td> <td>Sequence 10119, A</td>	US-60-167-167-10119	Sequence 10119, A
20 <td>47 <th>58.8</th> <td>325</td> <td>24 <td>US-60-191-637-10148</td> <td>Sequence 10148, A</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>24 <td>US-60-191-637-10148</td> <td>Sequence 10148, A</td> </td>	58.8	325	24 <td>US-60-191-637-10148</td> <td>Sequence 10148, A</td>	US-60-191-637-10148	Sequence 10148, A
21 <td>47 <th>58.8</th> <td>325</td> <td>24 <td>US-60-191-637-10148</td> <td>Sequence 10148, A</td> </td></td>	47 <th>58.8</th> <td>325</td> <td>24 <td>US-60-191-637-10148</td> <td>Sequence 10148, A</td> </td>	58.8	325	24 <td>US-60-191-637-10148</td> <td>Sequence 10148, A</td>	US-60-191-637-10148	Sequence 10148, A
22 <td>46 <th>57.5</th></td> <td>831</td> <td>19 <td>US-09-583-110-4287</td> <td>Sequence 4287, A</td> </td>	46 <th>57.5</th>	57.5	831	19 <td>US-09-583-110-4287</td> <td>Sequence 4287, A</td>	US-09-583-110-4287	Sequence 4287, A
23 <td>45 <th>56.2</th></td> <td>863</td> <td>19 <td>PCT-US01-08631-38846</td> <td>Sequence 38846, A</td> </td>	45 <th>56.2</th>	56.2	863	19 <td>PCT-US01-08631-38846</td> <td>Sequence 38846, A</td>	PCT-US01-08631-38846	Sequence 38846, A
24 <td>45 <th>55.0</th></td> <td>169</td> <td>1 <td>PCT-US97-02318-304</td> <td>Sequence 304, A</td> </td>	45 <th>55.0</th>	55.0	169	1 <td>PCT-US97-02318-304</td> <td>Sequence 304, A</td>	PCT-US97-02318-304	Sequence 304, A
25 <td>44 <th>55.0</th></td> <td>169</td> <td>13 <td>US-08-904-470-304</td> <td>Sequence 304, A</td> </td>	44 <th>55.0</th>	55.0	169	13 <td>US-08-904-470-304</td> <td>Sequence 304, A</td>	US-08-904-470-304	Sequence 304, A
26 <td>44 <th>55.0</th></td> <td>328</td> <td>21 <td>US-08-189-112-8340</td> <td>Sequence 8340, A</td> </td>	44 <th>55.0</th>	55.0	328	21 <td>US-08-189-112-8340</td> <td>Sequence 8340, A</td>	US-08-189-112-8340	Sequence 8340, A
27 <td>44 <th>55.0</th></td> <td>354</td> <td>24 <td>US-60-172-164-7681</td> <td>Sequence 948, A</td> </td>	44 <th>55.0</th>	55.0	354	24 <td>US-60-172-164-7681</td> <td>Sequence 948, A</td>	US-60-172-164-7681	Sequence 948, A
28 <td>44 <th>55.0</th></td> <td>354</td> <td>24 <td>US-60-191-637-9927</td> <td>Sequence 9527, A</td> </td>	44 <th>55.0</th>	55.0	354	24 <td>US-60-191-637-9927</td> <td>Sequence 9527, A</td>	US-60-191-637-9927	Sequence 9527, A
29 <td>44 <th>55.0</th></td> <td>354</td> <td>24 <td>US-60-191-681-7424</td> <td>Sequence 7424, A</td> </td>	44 <th>55.0</th>	55.0	354	24 <td>US-60-191-681-7424</td> <td>Sequence 7424, A</td>	US-60-191-681-7424	Sequence 7424, A
30 <td>44 <th>55.0</th></td> <td>867</td> <td>21 <td>US-09-711-164-357</td> <td>Sequence 357, A</td> </td>	44 <th>55.0</th>	55.0	867	21 <td>US-09-711-164-357</td> <td>Sequence 357, A</td>	US-09-711-164-357	Sequence 357, A
31 <td>44 <th>55.0</th></td> <td>867</td> <td>24 <td>US-60-164-415-357</td> <td>Sequence 357, A</td> </td>	44 <th>55.0</th>	55.0	867	24 <td>US-60-164-415-357</td> <td>Sequence 357, A</td>	US-60-164-415-357	Sequence 357, A
32 <td>44 <th>55.0</th></td> <td>867</td> <td>24 <td>US-60-112-584-8228</td> <td>Sequence 8228, A</td> </td>	44 <th>55.0</th>	55.0	867	24 <td>US-60-112-584-8228</td> <td>Sequence 8228, A</td>	US-60-112-584-8228	Sequence 8228, A
33 <td>43 <th>53.8</th> <td>213</td> <td>24 <td>US-60-06831-07283</td> <td>Sequence 628, A</td> </td></td>	43 <th>53.8</th> <td>213</td> <td>24 <td>US-60-06831-07283</td> <td>Sequence 628, A</td> </td>	53.8	213	24 <td>US-60-06831-07283</td> <td>Sequence 628, A</td>	US-60-06831-07283	Sequence 628, A
34 <td>43 <th>53.8</th> <td>424</td> <td>16 <td>PCT-US01-08631-48053</td> <td>Sequence 7158, A</td> </td></td>	43 <th>53.8</th> <td>424</td> <td>16 <td>PCT-US01-08631-48053</td> <td>Sequence 7158, A</td> </td>	53.8	424	16 <td>PCT-US01-08631-48053</td> <td>Sequence 7158, A</td>	PCT-US01-08631-48053	Sequence 7158, A
35 <td>43 <th>53.8</th> <td>856</td> <td>16 <td>US-09-252-651C-7158</td> <td>Sequence 7158, A</td> </td></td>	43 <th>53.8</th> <td>856</td> <td>16 <td>US-09-252-651C-7158</td> <td>Sequence 7158, A</td> </td>	53.8	856	16 <td>US-09-252-651C-7158</td> <td>Sequence 7158, A</td>	US-09-252-651C-7158	Sequence 7158, A
36 <td>43 <th>53.8</th> <td>906</td> <td>1 <td>PCT-US01-08631-48680</td> <td>Sequence 48680, A</td> </td></td>	43 <th>53.8</th> <td>906</td> <td>1 <td>PCT-US01-08631-48680</td> <td>Sequence 48680, A</td> </td>	53.8	906	1 <td>PCT-US01-08631-48680</td> <td>Sequence 48680, A</td>	PCT-US01-08631-48680	Sequence 48680, A
37 <td>43 <th>53.8</th> <td>1090</td> <td>1 <td>PCT-US01-08631-48053</td> <td>Sequence 48053, A</td> </td></td>	43 <th>53.8</th> <td>1090</td> <td>1 <td>PCT-US01-08631-48053</td> <td>Sequence 48053, A</td> </td>	53.8	1090	1 <td>PCT-US01-08631-48053</td> <td>Sequence 48053, A</td>	PCT-US01-08631-48053	Sequence 48053, A
38 <td>43 <th>53.8</th> <td>1090</td> <td>1 <td>PCT-US01-08631-48690</td> <td>Sequence 48690, A</td> </td></td>	43 <th>53.8</th> <td>1090</td> <td>1 <td>PCT-US01-08631-48690</td> <td>Sequence 48690, A</td> </td>	53.8	1090	1 <td>PCT-US01-08631-48690</td> <td>Sequence 48690, A</td>	PCT-US01-08631-48690	Sequence 48690, A
39 <td>43 <th>53.8</th> <td>1090</td> <td>1 <td>US-09-489-039A-9864</td> <td>Sequence 9864, A</td> </td></td>	43 <th>53.8</th> <td>1090</td> <td>1 <td>US-09-489-039A-9864</td> <td>Sequence 9864, A</td> </td>	53.8	1090	1 <td>US-09-489-039A-9864</td> <td>Sequence 9864, A</td>	US-09-489-039A-9864	Sequence 9864, A
40 <td>42 <th>52.5</th></td> <td>868</td> <td>18 <td>US-09-489-039A-9864</td> <td>Sequence 9864, A</td> </td>	42 <th>52.5</th>	52.5	868	18 <td>US-09-489-039A-9864</td> <td>Sequence 9864, A</td>	US-09-489-039A-9864	Sequence 9864, A
41 <td>42 <th>52.5</th></td> <td>868</td> <td>18 <td>US-09-489-039A-9864</td> <td>Sequence 9864, A</td> </td>	42 <th>52.5</th>	52.5	868	18 <td>US-09-489-039A-9864</td> <td>Sequence 9864, A</td>	US-09-489-039A-9864	Sequence 9864, A
42 <td>41 <th>51.2</th></td> <td>185</td> <td>24 <td>US-60-178-307-1864</td> <td>Sequence 1954, A</td> </td>	41 <th>51.2</th>	51.2	185	24 <td>US-60-178-307-1864</td> <td>Sequence 1954, A</td>	US-60-178-307-1864	Sequence 1954, A
43 <td>41 <th>51.2</th></td> <td>205</td> <td>1 <td>PCT-US01-08656-7196</td> <td>Sequence 7196, A</td> </td>	41 <th>51.2</th>	51.2	205	1 <td>PCT-US01-08656-7196</td> <td>Sequence 7196, A</td>	PCT-US01-08656-7196	Sequence 7196, A
44 <td>41 <th>51.2</th></td> <td>205</td> <td>1 <td>PCT-US01-08656-7196</td> <td>Sequence 7196, A</td> </td>	41 <th>51.2</th>	51.2	205	1 <td>PCT-US01-08656-7196</td> <td>Sequence 7196, A</td>	PCT-US01-08656-7196	Sequence 7196, A
45 <td>41 <th>51.2</th> <td>280</td> <td>24 <td>US-60-215-161-7865</td> <td>Sequence 7865, A</td> </td></td>	41 <th>51.2</th> <td>280</td> <td>24 <td>US-60-215-161-7865</td> <td>Sequence 7865, A</td> </td>	51.2	280	24 <td>US-60-215-161-7865</td> <td>Sequence 7865, A</td>	US-60-215-161-7865	Sequence 7865, A

ALIGNMENTS

RESULT 1
PCT-US00-18152-63
Sequence 63, Application PCT/US00018152
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: GLYCOPROTEIN YI AND USSES THEREOF
FILE REFERENCE: 785,311,228 PCT/US00/018152
CURRENT FILING DATE: 2000-06-30
EARLIER FILING DATE: 09/05/01, 387
EARLIER APPLICATION NUMBER: 09/454,824
EARLIER FILING DATE: 12/6/99 09/345,468
EARLIER APPLICATION NUMBER: 09/345,468
NUMBER OF SEQ ID NOS: 72/0/99
SOFTWARE: ParseSeq for Windows Version 3.0
SEQ ID NO: 63
LENGTH: 14
TYPE: PPT
ORGANISM: Homo sapiens
PCT-US00-18152-63

Query Match 100.0%; Score 80; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
OY 1 DKWEAYITPCARDV 14
DB 1 DKWEAYITPCARDV 14

```

RESULT 2
US-09-610-118-63
? Sequence 10, Application US/09610118
? GENERAL INFORMATION:
? APPLICANT: Busfield, S.
? APPLICANT: Villaveal, J.
? APPLICANT: Jandrot-Perrus, M.
? APPLICANT: Vainchenker, W.
? APPLICANT: Gull, D.
? APPLICANT: Gull, M.
? APPLICANT: Kishinev, G.
? TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
? FILE REFERENCE: 7853-211
? CURRENT FILING DATE: US/09/610.118
? PRIOR APPLICATION NUMBER: 09/503.387
? PRIOR FILING DATE: 2/14/00
? PRIOR APPLICATION NUMBER: 09/454.824
? PRIOR FILING DATE: 12/6/99
? PRIOR APPLICATION NUMBER: 09/345.468
? PRIOR FILING DATE: 6/30/99
? NUMBER OF SEQ ID NOS: 72
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 63
? SEQ ID NO 64
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-610-118-63

```

```

Query Match
Best Local Similarity 100.0%; Score 80; DB 20; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKMEAYITPGADV 14
DB 1 DKMEAYITPGADV 14

RESULT 3
US-09-832-312-63
? Sequence 63, Application US/09832312
? GENERAL INFORMATION:
? APPLICANT: Busfield et al.
? TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
? FILE REFERENCE: 653-724
? CURRENT APPLICATION NUMBER: US/09/832.312
? CURRENT FILING DATE: 2001-06-09
? PRIOR APPLICATION NUMBER: 09/610.118
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: 09/503.387
? PRIOR FILING DATE: 2000-02-14
? PRIOR APPLICATION NUMBER: 09/454.824
? PRIOR FILING DATE: 12/6/99
? PRIOR APPLICATION NUMBER: 09/345.468
? PRIOR FILING DATE: 1999-06-30
? NUMBER OF SEQ ID NOS: 78
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 63
? SEQ ID NO 64
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-832-312-63

```

```

Query Match
Best Local Similarity 100.0%; Score 80; DB 22; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKMEAYITPGADV 14
DB 1 DKMEAYITPGADV 14

```

```

RESULT 4
US-09-213-103-10
? Sequence 10, Application US/09213103
? GENERAL INFORMATION:
? APPLICANT: Egan, Sean
? APPLICANT: Egan, Sean
? APPLICANT: Egan, Sean
? TITLE OF INVENTION: Mammalian Brainiac Genes
? FILE REFERENCE: 5609
? CURRENT FILING DATE: US/09/213.103
? PRIOR APPLICATION NUMBER: 1998-12-17
? EARLIER FILING DATE: 1997-12-17
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: Blastclust Ver. 2.0
? SEQ ID NO 10
? LENGTH: 111
? TYPE: PRT
? ORGANISM: Drosophila melanogaster
US-09-213-103-10

```

```

Query Match
Best Local Similarity 58.6%; Score 47; DB 16; Length 111;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DKMEAYITPGAF 12
DB 72 DKMEAYITPGAF 83

```

```

RESULT 5
US-09-049-022-3
? Sequence 3, Application US/09049022
? GENERAL INFORMATION:
? APPLICANT: SOPERT, DANIEL R.
? APPLICANT: SOPERT, DANIEL R.
? TITLE OF INVENTION: CARDIAC AND PANCREATIC PROTEIN AND GENE
? NUMBER OF SEQUENCES: 42
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: STERN, KESSLER, GOLDBSTEIN & FOX P.L.L.C.
? STREET: 1100 NEW YORK AVENUE, SUITE 600
? CITY: WASHINGTON
? STATE: DC
? COUNTRY: US
? ZIP: 20005-3934
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: GENSCAN Release #1.0, Version #1.30
? CURRENT APPLICATION NUMBER: US/09/049.022
? FILING DATE: Hewlett
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/042.855
? FILING DATE: 28-MAR-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: STERPE, ERIC K.
? REGISTRATION NUMBER: 36,688
? REFERENCE/DOCKET NUMBER: 1488 0620001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 371-2600
? TELEFAX: (202) 371-2540
? INFORMATION FOR PUBLICATION:
? SEQUENCE CHARACTERISTICS: 3:
? LENGTH: 323 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-09-049-022-3

```

```

Query Match          58.8%: Score 47; DB 14; Length 325;
Best Local Similarity 58.3%: Pred. No. 32;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DKMEAYITPGAF 12
       1:1 1:1 1:1 1:1
Db      228 DNMPPYVNAQAF 239

RESULT 6
PCT-US98-27049-5
; SEQUENCE: 10, Application PC/TUS9827049
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Dendriac and Brainiac-3
; FILE REFERENCE: pF464.PCT
; CURRENT FILING DATE: 1998-12-16/066,006
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/077,687
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/108,928
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-27049-5

Query Match          58.8%: Score 47; DB 1; Length 325;
Best Local Similarity 58.3%: Pred. No. 32;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DKMEAYITPGAF 12
       1:1 1:1 1:1 1:1
Db      229 DNMPPYVNAQAF 240

RESULT 7
PCT-US99-30452-3
; SEQUENCE 3, Application PC/TUS9930452
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Brainiac-5
; FILE REFERENCE: EP50.PCT
; CURRENT FILING DATE: 1999-12-20
; EARLIER APPLICATION NUMBER: 60/113,804
; EARLIER FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
PCT-US99-30452-3

Query Match          58.8%: Score 47; DB 1; Length 325;
Best Local Similarity 58.3%: Pred. No. 32;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DKMEAYITPGAF 12
       1:1 1:1 1:1 1:1
Db      229 DNMPPYVNAQAF 240

```

```

US-09-150-857-10
; SEQUENCE 10, Application US/09150857
; GENERAL INFORMATION:
; APPLICANT: Zhou, Jiahong
; APPLICANT: Tartaglier, Louis A.
; TITLE OF INVENTION: LEPTIN INDUCED GENES
; FILE REFERENCE: 07334/093001
; CURRENT FILING DATE: 1998-09-10
; EARLIER FILING DATE: 1998-09-10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-150-857-10

Query Match          58.8%: Score 47; DB 15; Length 325;
Best Local Similarity 58.3%: Pred. No. 32;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DKMEAYITPGAF 12
       1:1 1:1 1:1 1:1
Db      229 DNMPPYVNAQAF 240

RESULT 9
US-09-150-857-10
; SEQUENCE 10, Application US/09150857A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Jiahong
; APPLICANT: Tartaglier, Louis A.
; TITLE OF INVENTION: LEPTIN INDUCED GENES
; FILE REFERENCE: 07334/093001
; CURRENT FILING DATE: 1998-09-10
; EARLIER FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-150-857-10

Query Match          58.8%: Score 47; DB 15; Length 325;
Best Local Similarity 58.3%: Pred. No. 32;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DKMEAYITPGAF 12
       1:1 1:1 1:1 1:1
Db      229 DNMPPYVNAQAF 240

RESULT 10
US-09-195-896-10
; SEQUENCE 10, Application US/09195896
; GENERAL INFORMATION:
; APPLICANT: Tartaglier, Louis A.
; APPLICANT: Zhou, Jiahong
; TITLE OF INVENTION: LEPTIN INDUCED GENES
; FILE REFERENCE: 07334/109001
; CURRENT FILING DATE: 1998-09-10
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: US 60/108,379
; EARLIER FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 09/150,857
; EARLIER FILING DATE: 1998-09-10

```

```

: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 10
: LENGTH: 325
: TYPE: prt
: ORGANISM: Drosophila melanogaster
: US-09-155-656-10

```

Query Match	58.84	Score 47	DB 15	Length 325
Best local similarity	55.38	Pred. No.	32	
Matches	7	Conservative	2	Mismatches 3
				Indels 0
				Gaps 0
QY	1	DKMEATITQAP	12	
Db	229	DRMPPTVTAQAF	240	

```

RESULT      11
US-09-213-103-5 : Sequence US/09213103
GENERAL INFORMATION:
TITLE OF INVENTION: Brain, Sean
FILE NO.: 09213103
CURRENT APPLICATION NUMBER: US/09/213.103
CURRENT FILING DATE: 1998-12-17
EARLIER FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 14
SEQUENCE INFORMATION:
SEQ ID NO. 5
SDS: Melanin Var. 2.10
LENGTH: 325
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-213-103-5

```

Query Match	58.8%	Score 47,	DB 16;	Length 325;
Best Local Similarity	58.3%;	Pred. No. 32;		
Matches	7;	Conservative	3;	Mismatches 0; Gaps 0.
1 DKMENTIPGAF 12				
: :				
Db 229 DRMPYVTAGAF 240				

RESULT 12
US-09-213-364-5
Sequence 5, Application US/09213364
GENERAL INFORMATION:
APPLICANT: Eimer, Reinhard
FILE OF INVENTION: Dendritic and Brainiac-3
CURRENT APPLICATION NUMBER: US/09/213_364
CURRENT FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: 60/066_006
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/077_687
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/108_928
EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 5: Patentin Var. 2.0
LENGTH: 325
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-364-5

Query Match	58.88;	Score 47;	DB 16;	Length 325;
Best Local, Similarity	58.38;	Pred. No. 32;		

	Matches	7. Conservative	2. Mismatches	3. Indels	0. Gaps
Qy	1	DKMEAYITTCGAF	12		
		I-I-I-I-I-I-I-I			
Db	229	DKMPPIYTAGAF	240		

```

RESULT 13
US-09-284-320-90
: Sequence 90, Application US/09284320
: GENERAL INFORMATION:
APPLICANT: Kato, Seishi et al.
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNASE
TITLE OF INVENTION: ENCODING THESE PROTEINS
PRIORITY REFERENCE: GIN-6703CJ05
CURRENT PRIORITY NUMBER: 05/09/284,320
PRIORITY FILING DATE: 1995-06-21
PRIORITY FILING DATE: 1995-06-21
PRIORITY FILING DATE: 1996-11-18
PRIORITY FILING DATE: 1996-11-18
PRIORITY FILING DATE: 1997-04/056
PRIORITY FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 2.0
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 325
TYPE: PRT
ORGANISM: Drosophila sp.
US-09-284-320-90

```

	Query Match	Score	47	DB	16	Length	325
Best Local Similarity	58.8%	Pred	No. 32,				
Matches	7	Conservative	2	Mismatches	3	Indels	0
							Caps 0
Oy	1	DKKRAYTGTGAF	12				
DB	229	DKKRAYTGTGAF	240				

```

1  RESULT:14
2  US-09-292-228-10
3  GENERAL INFO
4  APPLICATION: us/09292228
5  APPLICANT: White, David
6  APPLICANT: Zhou, Jiahang
7  APPLICANT: Tang, Louis A.
8  TITLE OF INVENTION: LEPTIN INDUCED GENES
9  PRIORITY NO.: 34,126,00 US/09/292-228
10 CURRENT FILING DATE: 1999-04-15
11 EARLIER APPLICATION NUMBER: US-09/195-896
12 EARLIER FILING DATE: 1998-11-19
13 EARLIER APPLICATION NUMBER: US-60/108-379
14 EARLIER APPLICATION NUMBER: US-60/108-379
15 EARLIER APPLICATION NUMBER: US-60/108-379
16 EARLIER FILING DATE: 1998-09-10
17 SOFTWARE: Seted for Windows Version 3.0
18 SD INCL NO: 105
19 SD INCL NO: 105
20 TYPE: PRT
21 ORGNAME: Diocophleia melanogaster
22 US-09-292-228-10

```

```

Query Match Similarity 58.8%; Score 47; DB 16; Length 35;
Best Local Similarity 55.3%; Pctd No. 32;
Matches 7; Conservative 3; Indels 0; Gaps 0;

Qy      1 DKWEATTTGAF 12
      |:|:|:|:|
Db      229 DKRPPTVTAAGF 240

```

```

RESULT 15
US-09-717-778-9
:
: GENERAL INFORMATION:
:
: APPLICANT: White, David W.
: APPLICANT: Zhou, Jiahong
: APPLICANT: Tartaglia, Louis A.
: APPLICANT: Stricker-Krongrad, Alain
: APPLICANT: Clausen, Henrik
: APPLICANT: UNKIND, JESSE
: FILE REFERENCE: 0734-11601
: CURRENT APPLICATION NUMBER: US/09/717,778
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: US 09/292,228
: PRIOR FILING DATE: 1999-04-15
: PRIOR APPLICATION NUMBER: US 09/195,896
: PRIOR FILING DATE: 1998-11-19
: PRIOR APPLICATION NUMBER: US 09/150,857
: PRIOR FILING DATE: 1998-09-10
: PRIOR APPLICATION NUMBER: US 60/106,378
: PRIOR FILING DATE: 1998-10-29
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 9
: LENGTH: 325
: TYPE: nt
: ORIGIN:
: Dirosophila melanogaster
US-09-717-778-9

```

```

Query Match      58.8% Score 47: DB 21: Length 325:
Best Local Similarity 58.3%: Pred. No. 32:
Matches 7: Conservative 2: Mismatches 3: Indels 0: Gaps 0:
Oy      1 DXXEATIRPGAF 12
      1:1 1:1 1:1 1:1
Db      229 DRMPYVTAGAF 240

```

Search completed: November 19, 2001, 08:23:15
 CPU time: 728 sec

THIS PAGE BLANK (USPTO)


```

? LENGTH: 221
? TYPE: PRG
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? OTHER INFORMATION: Inocyte ID No: 2636759CD1
US-09-976-594-664

```

```

Query Match          50.0% Score 40; DB 5; Length 221;
Best Local Similarity 63.6% Pred. No. 8.1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 4 EAYTPGADY 14
DB 31 EAYTPGADY 41

```

```

RESULT 3
US-09-815-242-5452
? Sequence 5452, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Trawick, John D.
? APPLICANT: Zyskind, Judith W.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes In
? FILE REFERENCE: ELITRA.011A
? CURRENT APPLICATION NUMBER: US/09/815.242
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-05-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 12382
? TYPE: PRG
? ORGANISM: Staphylococcus aureus
US-09-815-242-5452

```

```

Query Match          45.0% Score 36; DB 5; Length 209;
Best Local Similarity 70.0% Pred. No. 8.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 4 EAYTPGADY 13
DB 191 KAVITPGADY 200

```

```

RESULT 4
US-09-815-242-12382
? Sequence 12382, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Olsen, Karl L.

```

```

? APPLICANT: Zyskind, Judith W.
? APPLICANT: Trawick, John D.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes In
? FILE REFERENCE: ELITRA.011A
? CURRENT APPLICATION NUMBER: US/09/815.242
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 12382
? TYPE: PRG
? ORGANISM: Staphylococcus aureus
US-09-815-242-12382

```

```

Query Match          45.0% Score 36; DB 5; Length 209;
Best Local Similarity 70.0% Pred. No. 8.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 4 EAYTPGADY 13
DB 191 KAVITPGADY 200

```

```

RESULT 5
US-09-815-242-12980
? Sequence 12980, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Olsen, Karl L.
? APPLICANT: Zyskind, Judith W.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes In
? FILE REFERENCE: ELITRA.011A
? CURRENT APPLICATION NUMBER: US/09/815.242
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308

```



```

? PRIOR FILLING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO: 12668
? LENGTH: 209
? TYPE: PRT
? ORGANISM: Staphylococcus aureus
US-09-615-242-12980

Query Match      45.0%: Score 36; DB 5; Length 209;
Best Local Similarity 70.0%; Pct Ident 8.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      4 EAYITPGAD 13
        :|:|||||:
DB      191 KAVITPGAD 200

RESULT 6
US-09-615-242-5697
? Sequence 5697, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Ohlsen, Karl E.
? APPLICANT: Zyskind, Judith W.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? TITLE OF INVENTION: Proteolyses
? CURRENT APPLICATION NUMBER: US/09/815,242
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/407,727
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2000-03-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 5697
? LENGTH: 794
? TYPE: PRT
? ORGANISM: Staphylococcus aureus
US-09-615-242-5697

Query Match      45.0%: Score 36; DB 5; Length 794;
Best Local Similarity 45.5%; Pct Ident No. 35;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY      3 WEAITPGAD 13
DB      427 WATVITPGTE 437

RESULT 7
US-09-615-242-12668
? Sequence 12668, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert

```

```

? APPLICANT: Ohlsen, Karl E.
? APPLICANT: Zyskind, Judith W.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? TITLE OF INVENTION: Proteolyses
? FILE REFERENCE: EUTRA OLA US/09/815,242
? CURRENT FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/407,727
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2000-03-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 12668
? LENGTH: 802
? TYPE: PRT
? ORGANISM: Staphylococcus aureus
US-09-615-242-12668

Query Match      45.0%: Score 36; DB 5; Length 802;
Best Local Similarity 45.5%; Pct Ident No. 35;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY      3 WEAITPGAD 13
DB      427 WATVITPGTE 437

RESULT 8
US-09-897-516-6199
? Sequence 6199, Application US/09897516
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Ohlsen, Karl E.
? APPLICANT: Zyskind, Judith W.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? TITLE OF INVENTION: Proteolyses
? FILE REFERENCE: 38-21(51847)B
? CURRENT FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: US/09/897,516
? PRIOR FILING DATE: 2000-06-30
? NUMBER OF SEQ ID NOS: 8409
? SEQ ID NO 329
? LENGTH: 329
? TYPE: PRT
? ORGANISM: Xenorhabdus sp.
US-09-897-516-6199

Query Match      44.4%: Score 35.5; DB 5; Length 329;
Best Local Similarity 46.7%; Pct Ident No. 16;
Matches 7; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

```

OY 1 DKM---EAYTTCGAF 12
DB 163 DKMTOEHTVSSAK 177

RESULT 9

US-09-815-242-11391
Sequence 11391, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Yamamoto, Robert T.
APPLICANT: Ohlssen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Ohlssen, Karl L.
TITLE OF INVENTION: Identification of Essential Genes In
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815.242
PRIORITY FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/106,848
PRIORITY FILING DATE: 2000-05-25
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-22/257,931
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTEST for Windows Version 4.0
SEQ ID NO 11391
LENGTH: 944
TYPE: PRF
ORGANISM: Helicobacter pylori
US-09-815-242-11391

Query Match 44.8% Score 35.5; DB 5; Length 944;
Best Local Similarity: 63.8%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
OY 1 DKMAYTTCGAF 10
DB 491 DKMAYTTCGAF 501

RESULT 10

US-09-897-515-5275
Sequence 5275, Application US/09897515
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Karsenti-Gatfield, Karina C.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spitidnov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
CURRENT APPLICATION NUMBER: US/09/897.516
PRIORITY FILING DATE: 2001-05-28
PRIORITY APPLICATION NUMBER: US 60/215, 161
PRIORITY FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 5275
LENGTH: 359
TYPE: PRF
ORGANISM: Xenorhabdus sp.
US-09-897-515-5275

Query Match

43.8% Score 35; DB 5; Length 359;
Best Local Similarity: 58.3%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 DKMAYTTCGAFD 13

DB 179 DKMAYTTCGAFD 190

RESULT 11

US-09-815-242-5284
Sequence 5284, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Yamamoto, Robert T.
APPLICANT: Ohlssen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Ohlssen, Karl L.
TITLE OF INVENTION: Identification of Essential Genes In
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815.242
PRIORITY FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/106,848
PRIORITY FILING DATE: 2000-05-25
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-22/257,931
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTEST for Windows Version 4.0
SEQ ID NO 5284
LENGTH: 320
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-09-815-242-5284

Query Match 43.8% Score 35; DB 5; Length 390;
Best Local Similarity: 53.8%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 DKMAYTTCGAFD 13

DB 65 DKMAYTTCGAFD 77

RESULT 12

US-09-815-242-12599
Sequence 12599, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlssen, Karl L.
APPLICANT: Zyskind, Judith W.

```

? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John D.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xuh, Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? FILE REFERENCE: ELITRA-011A
? CURRENT APPLICATION NUMBER: US/09/815,242
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 12599
? LENGTH: 388
? TYPE: PRT
? ORGANISM: Staphylococcus aureus
US-09-815-242-12599

```

```

Query Match 43.88; Score 35; DB 5; Length 398;
Best Local 7; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 DMEAVITTPGAPD 13
 1:111:111
 Db 72 DEAVATYKVED 84

```

```

RESULT 13
US-09-815-242-10732
? Sequence 10732, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Ohlson, Karl L.
? APPLICANT: Zyskind, Judith W.
? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John D.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xuh, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? FILE REFERENCE: ELITRA-011A US/09/815,242
? CURRENT APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16

```

```

? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 10732
? LENGTH: 1149
? TYPE: PRT
? ORGANISM: Enterococcus faecalis
US-09-815-242-10732

```

```

Query Match 43.88; Score 35; DB 5; Length 1049;
Best Local Similarity 46.28; Pred. No. 70;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 KMEAVITTPGAFDV 14
 1:111:111
 Db 538 KRESYIDRAVFEV 550

```

```

RESULT 14
US-09-815-242-10119
? Sequence 10119, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Ohlson, Karl L.
? APPLICANT: Zyskind, Judith W.
? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John D.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xuh, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? FILE REFERENCE: ELITRA-011A US/09/815,242
? CURRENT APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 10119
? LENGTH: 244
? TYPE: PRT
? ORGANISM: Escherichia coli
US-09-815-242-10119

```

```

Query Match 42.58; Score 34; DB 5; Length 244;
Best Local Similarity 50.08; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 DMEAVITTPGAP 12
 1:111:111
 Db 38 DMKNATVATGAT 49

```

```

RESULT 15
US-09-815-242-10035
? Sequence 10035, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Ohlson, Karl L.

```

```

? APPLICANT: Zyskind, Judith W.
? APPLICANT: Melli, Daniel
? APPLICANT: Trevelock, John D.
? APPLICANT: Giese, Robert T.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes In
? FILE REFERENCE: ELITRA, 011A
? PUBLICATION NUMBER: US/09/815,242
? CURRENT FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/151,078
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ. INDS: 1110
? SOFTWARE: PatisSeq for Windows Version 4.0
? SEQ ID NO 10035
? LENGTH: 347
? TYPE: PRT
? ORGANSIM: Escherichia coli
? US-09-610-242-10035

```

```

Query Match      42.5%  Score 34:  DB 5:  Length 347,
Best Local Similarity 35.7%  Pred. No. 31:
Matches 5:  Conservative 5:  Mismatches 4:  Indels 0:  Gaps 0:
OY      1 DKMAYTTPQARDV 14
Db      82 EEMQAFINNSADV 95

```

Search completed: November 19, 2001, 08:23:31
 Job Time: 743 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM, protein - protein search, using sw model

Run on: November 19, 2001, 08:13:24 ; Search time 43.5 Seconds
(without alignments)

Title: US-09-610-118-63

Sequence: 1 DKWEAYITPGAFDV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*

```

1: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5F.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCrUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result					ID	Description
No.	Score	Query Match	Length	DB		
1	47	58.9	3.5	2	US-08-065-967-7	Sequence 2, Appl
2	47	58.9	3.5	2	US-08-065-967-7	Sequence 2, Appl
3	41	51.2	3.63	4	US-08-923-297-4	Sequence 4, Appl
4	41	51.2	3.63	5	PCR-US96-06511-4	Sequence 4, Appl
5	41	51.2	4.11	4	US-09-070-356-6	Sequence 6, Appl
6	40	50.0	4.11	4	US-07-942-245-3.2	Sequence 6, Appl
7	40	50.0	4.17	1	US-07-942-245-3.6	Sequence 36, Appl
8	40	50.0	4.17	1	US-07-942-245-3.6	Sequence 36, Appl
9	40	50.0	4.17	1	US-07-942-245-3.6	Sequence 36, Appl
10	39	48.8	1.005	1	US-08-452-083-2	Sequence 2, Appl
11	38	47.5	1.17	2	US-08-452-083-2	Sequence 2, Appl
12	38	47.5	1.17	4	US-08-479-285-2	Sequence 2, Appl
13	38	47.5	1.33	2	US-08-822-028-6	Sequence 6, Appl
14	38	47.5	1.33	2	US-08-822-028-6	Sequence 30, Appl
15	38	47.5	1.33	4	US-08-479-285-6	Sequence 30, Appl
16	38	47.5	1.33	4	US-08-479-285-6	Sequence 30, Appl
17	38	47.5	1.34	6	521996511285-30	Patent No. 521996
18	38	47.5	1.34	6	US-08-832-028-10	Sequence 10, Appl
19	38	47.5	1.54	4	US-08-479-285-10	Sequence 10, Appl
20	38	47.5	1.50	2	US-08-400-115-2	Sequence 2, Appl
21	38	47.5	2.71	2	US-08-400-115-4	Sequence 4, Appl
22	38	47.5	2.88	3	US-08-212-740-2	Sequence 2, Appl
23	38	47.5	3.63	1	US-09-033-409-5	Sequence 5, Appl
24	38	47.5	3.63	1	US-08-468-961-7	Sequence 7, Appl
25	37	46.2	3.63	4	US-08-973-297-7	Sequence 7, Appl
26	37	46.2	3.63	5	PCR-US96-06511-7	Sequence 7, Appl

28	37	46.2	623.1	US-08-5327-838-2	Sequence 2, Appl 1
29	36	45.0	480.2	US-08-466-812-5	Sequence 2, Appl 1
30	36	45.0	480.2	US-08-590-563-5	Sequence 5, Appl 1
31	36	45.0	480.2	US-08-466-812-4	Sequence 5, Appl 1
32	36	45.0	480.2	US-08-590-563-7	Sequence 7, Appl 1
33	36	45.0	492.4	US-08-590-563-4	Sequence 4, Appl 1
34	36	45.0	492.4	US-08-590-563-7	Sequence 7, Appl 1
35	36	45.0	590.2	US-08-756-517-12	Sequence 12, Appl 1
36	36	45.0	1024.4	US-09-091-117-5	Sequence 5, Appl 1
37	35.5	44.4	446.4	US-08-928-2138-52	Sequence 52, Appl 1
38	35.5	44.4	213.9	US-08-928-2138-60	Sequence 60, Appl 1
39	32	43.8	385.1	US-08-471-052A-118	Sequence 118, Appl 1
40	32	43.8	385.1	US-08-189-331-118	Sequence 118, Appl 1
41	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
42	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
43	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
44	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
45	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
46	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
47	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
48	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
49	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
50	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
51	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
52	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
53	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
54	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
55	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
56	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
57	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
58	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
59	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
60	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
61	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
62	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
63	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
64	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
65	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
66	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
67	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
68	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
69	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
70	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
71	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
72	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
73	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
74	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
75	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
76	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
77	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
78	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
79	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
80	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
81	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
82	35	43.8	386.2	US-08-471-052A-118	Sequence 118, Appl 1
83	35	43.8	386.2	US-08-471-052A-118	

ALIGNMENTS

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

```

Query Match      58.8% Score 47; DB 2; Length 325;
Best Local Similarity 38.3%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DKMEAYITPGAF 12
Db      229 DKMEAYITPGAF 240

RESULT 2
US-08-488-961-4
; Sequence 4, Application US/08488961
; Patent No. 5606042
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel S.
; APPLICANT: Walker, John C.
; TITLE OF INVENTION: Glycine and Phaseolus
; TITLE OF INVENTION: alpha-D-galactosidases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Relating, Etchington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; ZIP: 48069-4390
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/488,961
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; TELECOMMUNICATION:
; TELEPHONE: (810) 689-4070
; TELEFAX: (810) 689-3500
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-488-961-4

Query Match      51.2% Score 41; DB 1; Length 363;
Best Local Similarity 46.2%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DKMEAYITPGAF 13
Db      201 DKMAYVAGPGMN 213

RESULT 3
US-08-973-297-4
; Sequence 4, Application US/08973297
; Patent No. 6184017
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel S.
; APPLICANT: Walker, John C.
; TITLE OF INVENTION: Glycine and Phaseolus
; TITLE OF INVENTION: alpha-D-galactosidases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6184017Western Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION NUMBER: PCT/US96/06511
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; TELECOMMUNICATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5050
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids

```

```

; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,297
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; TELECOMMUNICATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5050
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-973-297-4

Query Match      51.2% Score 41; DB 4; Length 363;
Best Local Similarity 46.2%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DKMEAYITPGAF 13
Db      201 DKMAYVAGPGMN 213

RESULT 4
PCT-US96-06511-4
; Sequence 4, Application PCT/US9606511
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel S.
; APPLICANT: Walker, John C.
; TITLE OF INVENTION: Glycine and Phaseolus
; TITLE OF INVENTION: alpha-D-galactosidases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 Northwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06511
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; TELECOMMUNICATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5050
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids

```

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-0936-06511-4

Query Match 51.2%; Score 41; DB 5; Length 363;
Best Local Similarity 46.2%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 DKWEATITGCAED 13
DB 201 DKMASTAGPGCMN 213

RESULT 5
US-09-070-356-6
Sequence 6, Application US/09070356
Patent No. 6228631
GENERAL INFORMATION:
APPLICANT: Jack Goldstein
TITLE OF INVENTION: Recombinant a-N-
TITLE OF INVENTION: Acetylglucosaminidase
TITLE OF INVENTION: Enzyme and cDNA Encoding
TITLE OF INVENTION: Said Enzyme
NUMBER OF SEQUENCES: 7
SEQUENCE IDENTIFIERS:
ADDRESS: Amersham Biotechnology & Ebenstein
STREET: 90 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070_356
CLASSIFICATION:
PRIORITY DATA:
APPLICATION NUMBER: 08/037,248
FILING DATE: March 26, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pesquini, Patricia A.
REGISTRATION NUMBER: 34,894/45/12
REGISTRATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: no
HYPOTHETICAL: yes
ANTI-SENSE: yes
ORIGIN: yes
ORIGINAL SOURCE:
ORGANISM: guar plant *Cyamopsis tetragonoloba*
STRAIN: individual isolate:
DEVELOPMENTAL STAGE:
HAILOTYPE:
TISSUE TYPE:
CELL TYPE:

CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: library
SOURCE: unknown
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: guar a-galactosidase

IDENTIFICATION METHOD:
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Overbeke et al
TITLE: Cloning and Nucleotide Sequence of
Patent No. 6228631

TITLE: the a-galactosidase cDNA from
TITLE: *Cyamopsis tetragonoloba* (guar)
VOLUME: 13
PAGES: 541-550
DATE: 1989

DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-070-356-6

Query Match 51.2%; Score 41; DB 4; Length 411;
Best Local Similarity 46.2%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 DKWEATITGCAED 13
DB 248 DKMASTAGPGCMN 260

RESULT 6
US-07-942-245-12
Sequence 32 Application US/07942245
Patent No. 5636641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESS: Sughrue, Mton, Zlunn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 workstation
OPERATING SYSTEM: UNIX
SOFTWARE: in house
ORIGIN: yes
ORIGINAL SOURCE:
ORGANISM: *Cyamopsis tetragonoloba*
STRAIN: individual isolate:
DEVELOPMENTAL STAGE:
HAILOTYPE:
TISSUE TYPE:
CELL TYPE:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: no
HYPOTHETICAL: yes
ANTI-SENSE: yes
ORIGIN: yes
ORIGINAL SOURCE:
ORGANISM: guar plant *Cyamopsis tetragonoloba*
STRAIN: individual isolate:
DEVELOPMENTAL STAGE:
HAILOTYPE:
TISSUE TYPE:
CELL TYPE:

```

; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-32

```

```

Query Match      50.0%   Score 40: DB 1:   Length 117,
Best Local Similarity 46.2%   Pred. No. 12;
Matches      6:   Conservative 4;   Mismatches 3;   Indels 0;   Gaps 0;

QY      2 KWEATYTPGAEVY 14
      : : : : : : : : : :
Db      46 EHWATISSGSFT 58

```

RESULT 7
US-07-942-245-36
; Sequence 36, Application US/07942245
; Patent No. 5639641

[illegible]

1 APPLICANT: SEARLE, Stephen M.J.
2 APPLICANT: REES, Anthony R.
3 APPLICANT: ROCHKA, Michael A.
4 APPLICANT: ROY, Raymond C.
5 TITLE OF INVENTION: ANTIBODY VERNERING OF RODENT
6 TITLE OF INVENTION: ANTIBODIES
7 NUMBER OF SEQUENCES: 522
8 CORRESPONDENCE ADDRESS:
9 ADDRESS: Sughine, Mton, 21mm, Macpeak 6 Seas
10 STREET: 2100 Pennsylvania Avenue, N.W.
11 STATE: Washington
12 COUNTRY: D. United States
13 ZIP: 20037-1502
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: HP 9000/700 workstation
17 OPERATING SYSTEM: UNIX
18 SOFTWARE: In house
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/07/942,245
21 FILING DATE: 09
22 CLASSIFICATION: 530
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (202) 293-7060
25 TELEFAX: (202) 293-7860
26 TELEX: 6491103
27 INFORMATION FOR SEQ ID NO: 38:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 117
30 TYPE: amino acid
31 TOPOLOGY: linear
32
33 MOLECULE TYPE: peptide
34
35 US-07-942-245-38

Query Match: 50.0%; Score 40; DB 1; Length 117;
 Best Local Similarity 46.2%; Pred. No. 12;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 2 KWEATVPKAPRV 14
 : 111: 1:1:
 DB 46 EMVAVYSSGFTI 58
 RESULT 9
 US-08-455-386-11
 Sequence 11 Application US/08/565386
 Patent No. 5741697
 GENERAL INFORMATION:
 APPLICANT: HASLA, Patrick M.
 TITLE OF INVENTION: NACTHIOPEPTIDE OF CHLAMYDIA PSITTACI
 NUMBER OF SEQUENCES: 23
 CORRESPONDING ADDRESSES:
 ADDRESSER: MIXX
 STREET: Clinton Square, P.O. Box 1051
 CITY: Roches
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE SYSTEM: Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/565,386
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Susan J. 4.103
 REGISTRATION NUMBER: 176/00040
 REFERENCE/DOCKET NUMBER:
 TELEPHONE: 716-263-1636

TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
STRANDS: 1
STATUS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-565-386-11

Query Match 48.88; Score 39; DB 1; Length 596;
Best Local Similarity 46.08; P-Id No. 93;
Matches 6; Conservative 2; Mismatches 2; Gaps 0;

Oy 1 DKEAVITPC 10
Db 94 DNWESPTGG 103

RESULT 10
US-08-452-083-2
Sequence 2, Application US/08452083
Patent No. 5756327
GENERAL INFORMATION:
APPLICANT: Salsanfar, Mandana
APPLICANT: Schimmel, Paul R
TITLE OF INVENTION: RECOMBINANT MYOGLOBIN-TOPOGRAPHICAL ISOLEUCYL-TRNA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/305,765
FILING DATE: 13-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVID E., 22, 592
REGISTRATION NUMBER: C-37, 075C
TELEPHONE: (617) 861-6240
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-9540
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-452-083-2

Query Match 48.88; Score 39; DB 1; Length 1045;
Best Local Similarity 46.28; P-Id No. 16402;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DKEAVIT 8
Db 144 DEMOAVT 151

RESULT 11
US-08-822-028-2
Sequence 2, Application US/08822028
Patent No. 595811
GENERAL INFORMATION:
APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, MI KER
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLLOM, JEFFREY
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
STATE: MIDLAND
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34, 941
REFERENCE/DOCKET NUMBER: C-37, 075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-822-028-2

Query Match 47.58; Score 38; DB 2; Length 117;
Best Local Similarity 46.28; P-Id No. 26;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 KWEAVITGCAFDV 14
Db 65 EWICVTSRGNDI 77

RESULT 12
US-08-479-285-2
Sequence 2, Application US/08479285
Patent No. 6207815
GENERAL INFORMATION:
APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, MI KER
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:

```

ADDRESSER: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,285
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-285-2

Query Match
Best Local Similarity 47.5%; Score 38; DB 4; Length 117;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KWEATYTPARDY 14
DB 65 EMIGTISPRNDI 77

RESULT 13
US-08-822-028-6
Sequence 6; Application US/08822028
Patent No. 5993813
GENERAL INFORMATION:
INVENTOR: MEZES, PETER S
APPLICANT: GOURLE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, MI KERR
APPLICANT: RAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 133
TYPE: amino acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-822-028-30

```

```

APPLICATION NUMBER: US 08/040,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 133
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-822-028-6

Query Match
Best Local Similarity 47.5%; Score 38; DB 2; Length 133;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KWEATYTPARDY 14
DB 65 EMIGTISPRNDI 77

RESULT 14
US-08-822-028-30
Sequence 30; Application US/08822028
Patent No. 5993813
GENERAL INFORMATION:
INVENTOR: MEZES, PETER S
APPLICANT: GOURLE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, MI KERR
APPLICANT: RAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSER: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 133
TYPE: amino acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-822-028-30

```

Query Match 47.5%; Score 38; DB 2; Length 133;
 Best Local Similarity 46.2%; Pred.No. 30;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KWEATTPGAGPV 14
 : | | | | | :
 DB 65 EMIGYISPGNDI 77

RESULT 15

US-08-479-285-6
 : Sequence 6, Application US/08479285
 : Patent No. 6207815
 : GENERAL INFORMATION:
 : APPLICANT: MERS, PETER S
 : APPLICANT: GOURLIE, BRIAN B
 : APPLICANT: KAPLAN, DONALD A
 : APPLICANT: ANDERSON, JEFFREY
 : APPLICANT: SCHOLON, DONALD A
 : APPLICANT: KAPLAN, DONALD A
 : TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
 : NUMBER OF SEQUENCES: 74
 : MODIFIED ANTIBODIES FOR CANCER TREATMENT
 : CORRESPONDENCE ADDRESS: TUMER
 : TUMER, P O BOX 1967
 : STREET
 : CITY: MIDLAND
 : STATE: MICHIGAN
 : COUNTRY: USA
 : ZIP: 48641-1967
 : COMPUTER READABLE FORM:
 : COMPUTER FILE: floppy disk
 : COMPUTER LINK: compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentio Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/479,285
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 536
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: US 08/040687
 : FILING DATE: 31-MAR-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: TUMER, DUANE C
 : REGISTRATION NUMBER: 34,941
 : REFERENCE/DOCKET NUMBER: C-37, 075C
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 517-155-0104
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 133 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-479-285-6

Query Match 47.5%; Score 38; DB 4; Length 133;
 Best Local Similarity 46.2%; Pred.No. 30;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KWEATTPGAGPV 14
 : | | | | | :
 DB 65 EMIGYISPGNDI 77

Search completed: November 19, 2001, 08:13:25
 Job time: 138 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:14:21 ; Search time 48.99 Seconds
(without alignments) 20.214 Million cell updates/sec

Title: US-09-610-118-64

Sequence: 1 TRSSGSINAWYO 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Length	DB ID	Description
1	52	83.9	112 1	L6HU48
2	52	83.9	131 1	L6HU48
3	51	82.3	111 1	L6HU47
4	43	69.4	111 1	L6HU47
5	40	64.5	178 2	TR59047
6	38	61.3	502 1	L6HUKK
7	38	61.3	502 1	L6HUKK
8	38	61.3	556 2	HB2379
9	38	61.3	606 2	TR70772
10	38	61.3	726 2	CB85633
11	38	61.3	726 2	CB85633
12	37	59.7	108 2	PS00773
13	37	59.7	108 2	PS00773
14	37	59.7	108 2	PS00773
15	36	58.1	140 2	HB6592
16	36	58.1	352 2	TR76777
17	36	58.1	522 2	TR76777
18	36	58.1	539 2	BA91304
19	36	58.1	549 2	BA91304
20	36	58.1	997 2	TR15243
21	35	56.5	271 2	CB85633
22	35	56.5	271 2	CB85633
23	35	56.5	402 2	CB85633
24	35	56.5	503 1	TR15243
25	35	56.5	503 1	TR15243
26	35	56.5	512 1	TR15243
27	35	56.5	537 2	TR15243
28	35	56.5	541 2	TR15243
29	35	56.5	574 2	TR15243

30	35	56.5	1007 2	HB1670	conserved hypotet
31	35	56.5	1167 2	TR06146	disease resistance
32	34	54.8	57 2	PS00926	E2/NT18 protein (cd
33	34	54.8	72 2	137232	calcitonin gene-re
34	34	54.8	98 2	CS36048	Ig lambda chain -
35	34	54.8	124 2	C48234	hypothetical prote
36	34	54.8	127 2	C48234	calcitonin gene-re
37	34	54.8	127 2	C48234	Ig lambda chain pr
38	34	54.8	129 2	SR8058	Ig lambda chain pr
39	34	54.8	130 2	SR8057	Ig lambda chain pr
40	34	54.8	237 2	UC0799	nucleoside-specifi
41	34	54.8	294 2	DB8537	hypothetical prote
42	34	54.8	350 2	146608	MHC PD6-glycoprote
43	34	54.8	367 2	SS0621	SS081 protein - ye
44	34	54.8	396 2	T01049	hypothetical prote
45	34	54.8			

ALIGNMENTS

RESULT 1

L6HU48 Ig lambda chain V-VI region (Nlg-48) - human

C:Species: Homo sapiens (man)

C:Date: 28-Feb-1980 #sequence_revision 28-Feb-1980 #text_change 02-Sep-1997

J. Takayasu, N. Takayasu, T. Isobe, T. Shinoda, T. Okuyama, T. Shimizu, A.

A:Title: Comparative study on the structure of the light chains of human immunoglobulin

A:Reference number: A01991; MUID:80094390

A:Accession: A01991

A:Molecule type: protein

A:Keywords: This is a Dence Jones protein.

C:Comment: This is a Dence Jones protein.

C:Genetics:

A:Gene: GDB:IGLVE

A:Cross-References: GDB:119342; OMIM:147240

A:Map position: 22q11.2-22q11.2

C:Complex: An immunoglobulin heterodimer subunit consists of two identical light (L) chains and two identical heavy (H) chains. The light chains are associated into C:Keywords: heterodimer

F:15-93/Domain: Immunoglobulin homology <IMV>

F:22-91/Disulfide bonds: *status predicted

Query Match 83.9% Score 52; DB 1; Length 112;

Matches 11; Conservatively 8;6%; P1r4:0.013; 1; Indels 0; Gaps 0;

DB 23 TRSSGSINAWYO 35

11:1111111111

RESUME 2

L6HU48 Ig lambda chain precursor V-VI region (EB4) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997

C:Accession: A01990

R:Anderson, M.L.M.; Brown, L.; McKnight, E.; Kellow, J.E.; Young, B.D.

A:Title: Cloning and sequence analysis of an Ig lambda light chain mRNA expressed in

A:Reference number: A01990; MUID:85215660

A:Accession: A01990

A:Molecule type: mRNA

C:Genetics:

A:Gene: GDB:IGLVE

A:Cross-References: GDB:119342; OMIM:147240

Blochman, J. 195, 561-572, 1981
 A>Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light chain
 A:Reference number: A01987; MIMD:82091000
 A:Accession: A01987
 A:Molecule type: Protein
 A:Residues: 1-112 <LEU>
 A:Note: About half of the lambda chain C region is missing from this protein
 C:Comment: This protein was isolated from the spleen of a patient with myelodysplasia.
 C:Gene: CDB:IGLV8
 A:Cross-references: GDB:119342; OMIM:147240
 A:Map position: 22q11.2-22q11.2
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: amyloid; heterotrimer; immunoglobulin
 F:15-93/Domain: immunoglobulin homology <IMM>
 F:12-91/Disulfide bonds: 1status predicted

Query Match 61.3% Score 38; DB 1; Length 112;
 Best Local Similarity 61.5%; Pred. No. 5.6;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 TRSSGSIASNYV 13
 DB 23 TRSSGSIASNYV 35

RESULT 7

protein-tyrosine kinase (EC 2.7.1.112) hck - human
 C:Species: Homo sapiens (man)
 A:Accession: A27811; Genbank:revision 10-Nov-1995 #text_change 11-Jun-1999
 R:Gunterrell, N.; Lepo, R.; Varmus, H.; Bishop, J.M.; Pettinati, M.J.; Le Beau, M.M.; Die Mol. Cell. Biol. 7, 2267-2275, 1987
 A>Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and A:Accession: A27811; MIMD:87257942
 A:Molecule type: mRNA
 A:Residues: 1-505 <GU>
 A:Cross-references: GDB:M16591
 A:Note: The codon given for 3-Cys (TGC) is inconsistent with the authors' translation R:Ziegler, S.F.; Matlin, J.D.; Lewis, D.B.; Perlmutter, R.M.
 Mol. Cell. Biol. 7, 2276-2285, 1987
 A>Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of h A:Reference number: A27812; MIMD:87257943
 A:Molecule type: mRNA
 A:Residues: 1-505 <TIS>
 A:Cross-references: GDB:M16592; NID:AA52644.1; PID:g306833
 R:Hardelky, D.; Streibhardt, K.; Rudsamen-Walshmann, H.
 Gene 113, 275-280, 1992
 A>Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase A:Reference number: J01149; MIMD:92241880
 A:Molecule type: DNA
 A:Residues: 157-505 <HRA>
 A:Cross-references: EMBL:X59741
 R:Paranen, J.; Meekel, T.P.; Allitalo, R.; Lehtvasalho, H.; Allitalo, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
 A>Title: Novel tyrosine kinase gene expressed in K-562 human leukemia cells.
 A:Accession: A38286; MIMD:91602389
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 362-417 <PAR>
 C:Gene: GDB:HCK
 A:Cross-references: GDB:119303; OMIM:142370
 A:Map position: 20q11.20q12

A:Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
 C:Function: catalyzes the phosphorylation of a peptide/tyrosine residue by ATP
 A:Subcellular location: cytoplasm; nucleus
 C:Species: Arabidopsis thaliana (thale cress); protein kinase homology; SH2 homology; SH C:Keywords: ATP; autophosphorylation; blocked amino end; 11protein; myristylation; P:2-505/Product: protein-tyrosine kinase hck #status predicted <MKT>
 F:64-112/Domain: SH2 homology <SH2>
 F:123-270/Domain: SH2 homology <SH2>
 F:239-497/Domain: protein kinase homology <KIN>
 F:247-353/Region: protein kinase A binding motif
 F:347-424/Region: protein kinase A binding motif
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:369/Binding site: lys #status predicted
 F:199/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 61.3% Score 38; DB 1; Length 505;
 Best Local Similarity 61.7%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TRSSGSIASNYV 12
 DB 101 TRSSGSIASNYV 112

RESULT 8

conserved hypothetical protein VCA1085 [imported] - Vibrio cholerae (strain M16961 se C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 A:Accession: B82379
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.; Church, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Olin, H.; Dragol, I.; Sellers N. N. R. 406, 477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A:Reference number: A82035; MIMD:20406833
 A:Accession: B82379
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-558 <HRA>
 A:Cross-references: GDB:AE004434; GB:AE003853; NID:99558333; PID:AAFP6970.1; GSPDB:GN A:Experimental source: serogroup O1; strain M16961; biotype El Tor
 C:Gene: VCA1085
 A:Map position: 2
 Query Match 61.3% Score 38; DB 2; Length 556;
 Best Local Similarity 58.3%; Pred. No. 29;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 TRSSGSIASNYV 13
 DB 343 TRSSGSIASNYV 354

RESULT 9

hypothetical protein Y51A2D.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 A:Accession: Y51072
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z20307
 A:Accession: Y51072
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-606 <HRA>
 A:Cross-references: EMBL:AA071497; PID:CA16400.1; GSPDB:GN00023; CDS:Y51A2D.4
 C:Experimental source: clone Y51A2D

A:Gene: CESP:Y51A2D.4
A:Map position: 5
A:Introns: 4/3: 76/1: 226/3: 400/2: 446/1: 562/3
C:Superfamily: glucose transport protein

Query Match
Best Local Similarity 61.3%; Score 38; DB 2; Length 606;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSGSISANY 11
DB 442 TRUNSIANNYQ 452

RESULT 10
E85633
Hypothetical protein yccC [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Accession: E85633
C:Date: 12-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
R:Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasser, J.D.; Rose, D.J.; Mayhew
Natter, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamianos, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Status: preliminary
A:Status: preliminary
A:Status: preliminary
A:Residues: 1-726 <STO>
A:Cross-References: GR:AE005174; NID:q12514246; PIDN:AMG5529.1; CSPDB:GM00145; UWGP:Z13
A:Experimental source: strain O157:H7, substrain EDL933
C:Genes: yccC
A:Gene: yccC

Query Match
Best Local Similarity 61.3%; Score 38; DB 2; Length 726;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSGSISANY 13
DB 243 TRUNSIANNYQ 255

RESULT 11
E64839
Hypothetical protein yccC - Escherichia coli
C:Species: Escherichia coli
C:Accession: E64839
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2001
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1463, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: AB009595; MUID:97426017
A:Status: preliminary
A:Status: preliminary
A:Status: preliminary
A:Residues: 1-726 <LMAT>
A:Cross-References: GR:AE000200; GR:U00096; NID:92367111; PIDN:MAC74066.1; PID:q1787216;
C:Experimental source: Strain K-12, substrain MD1655
A:Gene: yccC
A:Gene: yccC
C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein
F:34-50/Domain: transmembrane #status predicted <TM>
F:428-444/Domain: transmembrane #status predicted <TM>
F:539-546/Region: nucleotide-binding motif A (P-loop)

Query Match
Best Local Similarity 61.3%; Score 38; DB 2; Length 726;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TRSGSISANY 13
DB 243 TRUNSIANNYQ 255

RESULT 12
R30073
I kappa chain V region (36C13 V2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: P50073
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearing
A:Reference number: A52781; MUID:89310348
A:Accession: P50073
A:Status: translation not shown
A:Status: translation not shown
A:Status: translation not shown
A:Residues: 1-108 <LEV>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-31/Domain: Immunoglobulin homology <IMH>

Query Match
Best Local Similarity 59.7%; Score 37; DB 2; Length 108;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RSSGSISANY 12
DB 24 RASSISANYL 34

RESULT 13
E59098
Hypothetical protein PKX1-61 - Bacillus anthracis virulence plasmid PKX1
C:Species: Bacillus anthracis
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 16-Feb-2001
C:Accession: E59098
R:Okimaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Kelm, P.; Koch
J. Bacteriol. 181, 6509-6515, 1999
A:Title: Sequence and organization of PKX1, the large Bacillus anthracis plasmid harb
A:Reference number: A59091; MUID:9945483
A:Accession: E59098
A:Status: preliminary
A:Status: preliminary
A:Status: preliminary
A:Residues: 1-336 <OKI>
A:Cross-References: GR:AF065404; NID:q4894216; PIDN:AM32365.1; PID:q4894277
A:Experimental source: Strain Sterne
A:Gene: PKX1-61
A:Gene: Plasmid
C:Superfamily: hypothetical protein PKX1-61

Query Match
Best Local Similarity 59.7%; Score 37; DB 2; Length 236;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RSSGSISANY 13
DB 25 KDSGSLLMYVE 36

RESULT 14
R30578
myosin IC - silene mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 08-Sep-2000
C:Accession: T30578
R:Peterson, M.D.; Novak, K.D.; Reedy, M.C.; Ruman, J.I.; Titus, M.A.
J. Cell Sci. 108, 1093-1103, 1995

A:Title: Molecular genetic analysis of myoc, a Dictyostelium myosin I.
 A:Reference number: Z20872; M0ID:95348228
 A:Accession: Z20872
 A:Status: preliminary
 A:Translation: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1181 <PEP>
 A:Cross-references: EMBL:L35323; NID:9532123; PID:9532124; PIDN:AN037427.1
 C:Genetics:
 A:Gene: myoc
 A:Introns: 307/1
 A:Suppl: 00111; protein myosin heavy chain 1B; myosin motor domain homology; SH3 homolo
 F:18-665/Domain: myosin motor domain homology <MO>

Query Match

59.7%; Score 37; DB 2; Length 1181;

Best Local Similarity 53.8%; Pred. No. 95;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 TRSSGSIASMYVQ 13

1:1:1:11111

DB 1167 TKQICMLPSMYVQ 1179

RESULT 15

H86292
 hypothetical protein AAF82154.1 [imported] - Arabidopsis thaliana
 C:Accession: H86292
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 R:Phenology: A: Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Jensen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408: 816-820, 2000
 A:Reference number: A86141; M0ID:21016719
 A:Accession: A86141
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-140 <STO>
 A:Cross-references: GB:AE005172; NID:98927663; PIDN:AAF82154.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match

58.1%; Score 36; DB 2; Length 140;

Best Local Similarity 88.9%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TRSSGSIAS 9

111111111

DB 56 TRSSGSIAS 64

Search completed: November 19, 2001, 08:14:22
 Job time: 195 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:25:35 ; Search time 27.32 Seconds

Title: US-09-610-118-64

Sequence: 1 TRSSGSIASNYVQ 13

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93433

```
Minimum DB seq length: 0
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_39: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. . . .

SUMMARIES

Result	Query				ID	Description
No.	Score	Match	Length	DB		
1	52	83.9	112	1	LV6C_HUMAN	P01722 homo sapien
2	52	83.9	112	1	LV6D_HUMAN	P06319 homo sapien
3	51	82.3	111	1	LV6C_HUMAN	P06318 homo sapien
4	43	69.4	111	1	LV6C_HUMAN	P06317 homo sapien
5	38	61.3	112	1	LV6A_HUMAN	P01721 homo sapien
6	38	61.3	526	1	HCK_HUMAN	P06631 homo sapien
7	38	61.3	726	1	ETK_ECOLI	P38143 escherichia
8	37	59.7	1181	1	MYSC_MTCD1	P44522 delyosetali
9	36	58.1	416	1	PNX1_HUMAN	P44523 xenopus lae
10	36	58.1	416	1	PNX1_HUMAN	P44524 xenopus lae
11	36	58.1	503	1	WNT3_HUMAN	P09498 homo sapien
12	35	56.5	511	1	LXR_HUMAN	P05645 mus muscu
13	35	56.5	524	1	HCK_MOUSE	P08103 mus muscu
14	35	56.5	531	1	FXR_XIPHE	P27446 xiphiophoru
15	35	56.5	541	1	VEA_MOUSE	P27436 mus muscu
16	35	56.5	574	1	CBPA_SCHPO	P04726 mus muscu
17	34	54.8	37	1	CBPA_PIG	P87311 schistosom
18	34	54.8	127	1	PAZ2_HUMAN	P30880 homo sapien
19	34	54.8	127	1	PAZ2_HUMAN	P30880 homo sapien
20	34	54.8	127	1	PAZ2_HUMAN	P30880 homo sapien
21	34	54.8	127	1	PAZ2_HUMAN	P30880 homo sapien
22	34	54.8	127	1	PAZ2_HUMAN	P30880 homo sapien
23	34	54.8	127	1	PAZ2_HUMAN	P30880 homo sapien
24	34	54.8	127	1	PAZ2_HUMAN	P30880 homo sapien
25	33	53.2	182	1	YMB4_ECOLI	P73866 escherichia
26	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
27	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
28	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
29	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
30	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
31	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
32	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
33	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
34	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
35	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
36	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
37	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
38	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
39	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
40	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
41	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
42	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
43	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
44	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
45	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
46	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
47	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
48	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
49	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
50	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
51	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
52	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
53	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
54	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
55	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
56	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
57	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
58	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
59	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
60	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
61	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
62	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
63	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
64	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
65	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
66	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
67	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
68	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
69	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
70	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
71	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
72	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
73	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
74	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
75	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
76	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
77	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
78	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
79	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
80	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
81	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
82	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
83	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
84	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
85	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
86	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
87	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
88	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
89	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
90	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
91	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
92	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
93	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
94	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
95	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
96	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
97	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
98	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
99	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu
100	33	53.2	186	1	PEBP_MOUSE	P10865 mus muscu

[illegible]

FT	MOD. RSS	21	411	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CONFLICT	44	24	S -> C (IN AA55644).
SO	SEQUENCE	526 AA:	59583 MW:	347E877A0A6412B3 CRC64:
QY	1 TRSSGSINSNV	12	61.7%	Score 38. DB 1:
Db	122 TRKESTPSNV	133	66.7%	Procd. No. 9-2:
			0:	Mismatches
			4:	Indels
			0:	Gaps
RESULT	7			
OC	ETK_ECOLI	STANDARD:	PRT:	726 AA.
AD	P8134:	P81579:		
IC	01-OCT-1994	(Rel. 30: Created)		
DT	01-OCT-1994	(Rel. 30: Last sequence update)		
DT	30-MAY-2000	(Rel. 30: Last sequence update)		
DE	TYROSINE-PROTEIN KINASE ETK (EC 2.7.1.112).			
GN	ETK.			
OC	Escherichia coli.			
OC	Bacteria: Proteobacteria: gamma subdivision: Enterobacteriaceae:			
OC	Bacterichia.			
OC	NCBI_TaxId=562:			
RP	SEQUENCE FROM N.A.			
RP	STRAIN-K12 / MG1655:			
RP	MEDLINE-97426617: PubMed-9278503:			
RP	Blattner F.R., Plunkett G. II, Bloch C.A., Ferna N.T., Burland V.,			
RP	Raley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RP	Gregor J., Davis N.W., Klapper H.A., Gooden M.A., Rose D.J.,			
RP	"The complete E. coli genome sequence of Escherichia coli K-12."			
RP	Science 277:1453-1474(1997).			
RP	(2)			
RP	SEQUENCE FROM N.A.			
RP	STRAIN-K12:			
RP	MEDLINE-97061203: PubMed-8905232:			
RP	Ohlme E., Alona H., Bohn T., Fujita K., Hayashi K., Honjo A.,			
RP	Klimke S., Kikuchi S., Kato T., Kajihara M., Kana K., Kashimoto K.,			
RP	Mori H., Motomura K., Nakamura Y., Nishimoto S., Nishitani T., Kizubuchi K.,			
RP	Sampel G., Seki Y., Toge H., Takemoto K., Wada C., Yamamoto Y.,			
RP	Yano M., Horikuchi T.			
RP	A 718-kb DNA sequence of the Escherichia coli K-12 genome			
RP	corresponding to the 12.7-28.0 min region on the linkage map."			
RP	Gen. Res. 5:137-155(1996).			
RP	(3)			
RP	SEQUENCE FROM N.A.			
RP	STRAIN-E2348/59:			
RP	Ilan O.A., Bloch V., Frankel G., Ullrich H., Gelder K., Rosenshine I.,			
RP	Protein-Lysine Kinase in bacterial pathogens are associated with			
RP	virulence and production of exopolysaccharide."			
RP	Submitted (Apr-1999) to the EMBL/Genbank/DBD databases.			
RP	SEQUENCE OF 628-726 FROM N.A.			
RP	MEDLINE-90386616: PubMed-2169385:			
RP	Dassa J., Marck C., Boquet P.L.:			
RP	"The complete nucleotide sequence of the Escherichia coli gene appA			
RP	glucose-1-phosphatase."			
RP	J. Bacteriol. 173:5497-5500(1990).			
RP	IDENTIFICATION:			
RP	MEDLINE-95075659: PubMed-798438:			
RP	Bogrodovsky M., Rud K.E., Koonin F.V.:			
RP	"Intrinsic and extrinsic approaches for detecting genes in a			
RP	bacterial genome."			
RP	Nucleic Acids Res. 22:4756-4767(1994).			
RP	"SIMILARITY: SOM: 22:4756-4767(1994).			
RP	"- SIMILARITY: SOM: 22:4756-4767(1994).			

```

CC -----
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use. However, the EMBL/EBI logo and this content is in no way to be
CC modified and this statement is not removed and you are not to
CC entitle requires a license agreement (see http://www.isb.sdb.ch/announcements/
CC of send an email to license@isb.sdb.ch).
CC -----
DR EMBL: A63004200, AAC74056.1, -
DR EMBL: A63004200, AAC74056.1, -
DR EMBL: A2338695, CAB3868.1, -
DR EMBL: M56708.7; NOT_ANNOTATED_CDS.
DR Ecocode: EC11826; etc.
KW Transference: tyrosine-protein kinase; Transmembrane.
FT TRANSMEM 33 53
FT VARIANT 92 92 Q -> L (IN STRAIN E2348/65).
FT VARIANT 92 92 E -> G (IN STRAIN E2348/65).
FT VARIANT 216 216 E -> L (IN STRAIN E2348/65).
FT CONFLICT 726 726 E -> RNN (IN REF. 5).
SQ SEQUENCE 726 AA: 81241 MW: 840605956800A22 CRC64;

```

```

RESULT      8
MYSC_DICD1 STANDARD;          PART; 1181 AA.
ID          AC
AC P43522.1985 (Rel. 32) Created
P43522.1985 (Rel. 32) Sequence update
DI 01-NOV-1995 (Rel. 32) Last annotation update
DT 15-JUL-1998 (Rel. 35) Last annotation update
DE MYOSIN IC HEAVY CHAIN
GN MYOC OR DMIC
OS Dictyostellium discoideum ( slime mold ).
OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostellium.
PC 1181
NCBI_TaxId=44689;
RP SEQUENCE FROM N.A.
RF STRAIN=AX2;
RX MEDLINE=95348278; PubMed=7623596;
RA Peterson M.D., Novak K.D., Reedey M.C., Ruman J.I., Tilus M.A.;
RT Molecular genetic analysis of myocA, a Dictyostellium myosin I.;
RL J. Cell Sci. 108:1093-1103(1995).
IL ACTIVITY: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE
CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC
CC -I- SUBUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED, DIMERS OF A HEAVY
CC AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO FILAMENTS
CC -I- SIMILARITY: BELONGS TO THE MYOSIN TYPE I FAMILY (SMALL MYOSINS).
CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC the European Bioinformatics Centre. There are no restrictions on its
CC use by non-profit institutions as long as they acknowledge the source of
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
CC -----
CC BBG: L03323; AKC3427.1 ;
CC DICTDB: DD01050.D; MYOC
CC InterPro: IPR001457; -
CC InterPro: IPR001609; -
CC Pfam: PF000018; SH3; 1.
CC Pfam: PF000063; myosin_head; 2.

```


CC EMBL: A0009799.1:2322..1.
 DR EMBL: A0009799.1:2322..1.
 DR EMBL: A0009799.1:2322..1.
 DR EMBL: A0009799.1:2322..1.
 DR EMBL: A0009799.1:2322..1.
 DR SDD: S0006149; CEST1.
 DR Hydrolyase: mRNA processing; mRNA capping; Nuclear protein.
 CC CONFLICT 242 242 R > R (IN REF. 2).
 SO SEQUENCE 549 AA; 61821 MW; D8A6GPEB7E027F9 CRC64;

 Query Match 58.18; Score 16; DB 1; Length 549;
 Best Local Similarity 60.08; Pred. No. 23;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

 Oy 3 SSGSIASNY 12
 Db 162 MEKMSHWI 171

 RESULT 11
 HCK_RAT STANDARD; PRT: 503 AA.
 ID HCK_RAT
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TYROSINE-PROTEIN KINASE HCK (PC 2.7.1.112) (P56-HCK) (HEMOPOIETIC CELL KINASE).
 GN HCK.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Oono Y., Sugimoto Y., Fukuko M., Matsui A., Nagata K.I., Nozawa Y.;
 RT Molecular cloning of rat cDNA encoding hck tyrosine kinase from
 RL Blochem. Biophys. Res. Commun. 181:1137-1144(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-NISTAR; TISSUE-Spleen;
 RA Vajda Dorit B.S., Rema V., Kamatkar S., Swarup G.;
 RT Characterization of a cDNA coding for rat hck tyrosine kinase and
 RL J. Biol. 19:117-128(1994).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE PC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRADATION PROCESS OF NEUTROPHILS.
 CC -1- PROMOTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH MEMBRANES.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
 CC THIS SWISS-PROT entry is a copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC use by non-profit institutions as long as its distribution on its
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.slb.ch).
 CC EMBL: S7141.1:180714..1.
 DR EMBL: M61665.1:180714..1.
 DR EMBL: M61665.1:180714..1.
 DR HSBP: P08631; 2HCK.
 DR InterPro: IPR000719; -.

DR InterPro: IPR000980; -.
 DR InterPro: IPR001245; -.
 DR InterPro: IPR001452; -.
 DR Pfam: PF00017; SH2 1.
 DR Pfam: PF00018; SH3 1.
 DR Pfam: PF00019; SH3 1.
 DR PRINTS: PR00109; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM_1.
 DR PROSITE: PS00011; SH2 1.
 DR PROSITE: PS00011; SH3 1.
 DR TRANSFASER: Tyrosine protein kinase; Phosphorylation; ATP-binding;
 KM Myristate; SH2 domain; SH3 domain; Alternative initiation.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 55 115 SH2.
 FT DOMAIN 121 218 SH2.
 FT DOMAIN 239 452 SH2.
 FT DOMAIN 452 452 SH2.
 FT BINDING 267 358 SH2.
 FT ACT SITE 356 358 SH2.
 FT MOD_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 51 51 F > V (IN REF. 2).
 FT CONFLICT 205 205 I -> T (IN REF. 2).
 FT CONFLICT 306 306 I -> T (IN REF. 2).
 SO SEQUENCE 503 AA; 57016 MW; A1RCF3F0EB2F7F9 CRC64;

 Query Match 56.54; Score 35; DB 1; Length 503;
 Best Local Similarity 58.38; Pred. No. 33;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

 Oy 1 TRSSSIASNY 12
 Db 99 TKKEITPSNY 110

 RESULT 12
 LYN_HUMAN STANDARD; PRT: 511 AA.
 ID LYN_HUMAN
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DT 10-MAY-2000 (Rel. 39, Last annotation update)
 DE TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112).
 GN LYN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-8712710; PubMed-3561390;
 RA Yamashita K.-I., Yamashita S.-I., Sema K., Sukegawa J., Miyajima N.,
 RA Yamashita K.-I., Yamashita S.-I., Toyoshima K.;
 RT Isolation and characterization of the cDNA for the gene encoding a possible tyrosine kinase
 RT similar to p56lck in a rat thymocyte cell line.
 RL Mol. Cell. Biol. 7:237-243(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94171041; PubMed-8125304;
 RA Alder L.G., Raben N., Miller B., Jelsma C.;
 RT The cDNA encoding two forms of the LYN protein tyrosine kinase are
 RT expressed in rat thymocytes, rat thymic cells and human myeloid cells.
 RL Gene 138:219-222(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP +
 CC -1- PROTEIN TYROSINE PHOSPHATE.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

RC	STRAIN-ICR; TISSUE=MACROPHAGE;	
RA	MEDLINE-9806781; PUBMED-3684607;	
RA	Klems M.J., McKercher S.R., Maki R.A.;	
RT	Genes and proteins of the human	
RT	Nucleolus. Semin Oncol. 1997;24(1):	
RM	Nucleolar Acta Res. 15;9600-9600(1987).	
RM	[2]	
RM	SEQUENCE OF 1-22 524 PPOX N.A.	
RA	MEDLINE-88068587; PUBMED-3117404;	
RA	Holzman D.A., Cook W.D., Dunn A.R.;	
RT	Isolation and sequence of a cDNA corresponding to a src-related gene	
RT	expressed in murine Hemopoietic cells	
RT	[3]	
RT	Natl. Acad. Sci. U.S.A. 84;8325-8329(1987).	
RP	SEQUENCE OF 1-22 FCN N.A., AND ALTERNATIVE INITIATION.	
RA	MEDLINE-91343656; PUBMED-1875927;	
RA	Lock P., Ralph S., Stanley E., Boullet I., Ramsay R.;	
RT	"Two isoforms of murine hck, generated by utilization of alternative	
RT	translational initiation codons, exhibit different patterns of	
RT	subcellular localization." J Biol Chem. 268(19):14019-14019(1993).	
CC	-1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC	
CC	RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO	
CC	CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE	
CC	DEGRANULATION PROCESS OF NEUTROPHILS.	
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +	
CC	PROTEIN TYROSINE PHOSPHATE.	
CC	-1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH	
CC	MEMBRANES OF GRANULOCYTES AND MONOCYTES.	
CC	-1- ALTERNATIVE PRODUCTS: THE P59-HCK AND P56-HCK ARE PRODUCED BY THE	
CC	USE OF ALTERNATIVE INITIATION SITES.	
CC	-1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE	
CC	MYELOID AND B-LYMPHOID LINEAGES.	
CC	-1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.	
CC	-1- SIMILARITY: NO OTHER KNOWN PROTEIN KINASES IN THE CATALYTIC	
CC	DOMAIN. ADPOSED TO THE SRC SUBFAMILY.	
CC	-----	
CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION	
CC	BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION U	
CC	THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON WA	
CC	USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY	
CC	MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY FOR COMMERCIAL	
CC	ENTITIES REQUIRES A LICENSE AGREEMENT (SEE http://www.lsb.slb.ch/announcement/	
CC	OR SEND AN EMAIL TO license@lsb.slb.ch).	
CC	EMBL: Y00487; CA668544.1; -	
CC	EMBL: J03023; AAA37305.1; -	
CC	PIR: A27282; TYMSHC.	
CC	PIR: A39973; A39973.	
CC	HSSP: P08631; ZHCK.	
DR	MSD; MGI:36052; HCK.	
DR	Interpro: IP000980.	
DR	Interpro: IP000980.	
DR	Interpro: IP001452; -	
DR	Interpro: IP001452; -	
DR	Pfam: PF00017; SH2; 1.	
DR	Pfam: PF00018; SH3; 1.	
DR	Pfam: PF00069; ptkinase; 1.	
DR	PRINTS: PR00109; TYRKINASE.	
DR	PRINTS: PR00152; SH2DOMAIN.	
DR	PRINTS: PR00152; SH2DOMAIN.	
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.	
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE: PS50002; SH3; 1.	
RM	TRANSFERASE: TYROSINE PROTEIN KINASE. PHOSPHORYLATION: ATP-BINDING;	
RM	CHAINS: SH2 DOMAIN; SH3 DOMAIN.	
FT	CHAIN 22 524	
FT	INTL_MET 22 22	
FT	LIPID 23 23	
FT	TYROSINE-PROTEIN KINASE P59-HCK.	
FT	FOR P56-HCK.	
FT	MYSTATATE (BY SIMILARITY).	
FT	MYSTATATE (BY SIMILARITY).	

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:25:02 : Search time 81.19 Seconds

(without alignments)
21.184 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNYQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 13205027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: SPREMBL_16:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_mammal:*
6: SP_invertebrate:*
7: SP_plant:*
8: SP_organella:*
9: SP_phage:*
10: SP_protist:*
11: SP_unclassified:*
12: SP_virus:*
13: SP_virus:*
14: SP_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	42	67.7	517	5 094879	094879 drosophila
2	42	67.7	517	5 094933	094933 drosophila
3	40	64.5	517	5 094933	094933 drosophila
4	39	63.3	519	3 013420	013420 drosophila
5	38	61.3	505	4 094933	094933 drosophila
6	38	61.3	519	3 013420	013420 drosophila
7	38	61.3	505	4 094933	094933 drosophila
8	38	61.3	519	3 013420	013420 drosophila
9	38	61.3	505	4 094933	094933 drosophila
10	38	61.3	519	3 013420	013420 drosophila
11	38	61.3	505	4 094933	094933 drosophila
12	38	61.3	519	3 013420	013420 drosophila
13	36	58.1	294	10 094879	094879 drosophila
14	36	58.1	308	10 094879	094879 drosophila
15	36	58.1	317	2 094879	094879 drosophila
16	36	58.1	352	5 027556	027556 caenorhabditis
17	36	58.1	352	5 027556	027556 caenorhabditis
18	36	58.1	352	5 027556	027556 caenorhabditis
19	36	58.1	352	5 027556	027556 caenorhabditis
20	36	58.1	352	5 027556	027556 caenorhabditis

20	35	56.5	132	14 097686	097686 human immunoglobulin
21	35	56.5	132	14 097686	097686 human immunoglobulin
22	35	56.5	132	14 097686	097686 human immunoglobulin
23	35	56.5	132	14 097686	097686 human immunoglobulin
24	35	56.5	132	14 097686	097686 human immunoglobulin
25	35	56.5	132	14 097686	097686 human immunoglobulin
26	35	56.5	132	14 097686	097686 human immunoglobulin
27	35	56.5	132	14 097686	097686 human immunoglobulin
28	35	56.5	132	14 097686	097686 human immunoglobulin
29	35	56.5	132	14 097686	097686 human immunoglobulin
30	35	56.5	132	14 097686	097686 human immunoglobulin
31	35	56.5	132	14 097686	097686 human immunoglobulin
32	35	56.5	132	14 097686	097686 human immunoglobulin
33	35	56.5	132	14 097686	097686 human immunoglobulin
34	35	56.5	132	14 097686	097686 human immunoglobulin
35	35	56.5	132	14 097686	097686 human immunoglobulin
36	35	56.5	132	14 097686	097686 human immunoglobulin
37	35	56.5	132	14 097686	097686 human immunoglobulin
38	35	56.5	132	14 097686	097686 human immunoglobulin
39	35	56.5	132	14 097686	097686 human immunoglobulin
40	35	56.5	132	14 097686	097686 human immunoglobulin
41	35	56.5	132	14 097686	097686 human immunoglobulin
42	35	56.5	132	14 097686	097686 human immunoglobulin
43	35	56.5	132	14 097686	097686 human immunoglobulin
44	35	56.5	132	14 097686	097686 human immunoglobulin
45	35	56.5	132	14 097686	097686 human immunoglobulin

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRG:	517 MA.
094879	094879		
AC	094879		
DT	01-FEB-1997 (TREMBLrel. 02, Created)		
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	DSRC41		
GN	SRG42A OR CG7B73.		
OS	Drosophila melanogaster (fruit fly)		
OC	Arthropoda; Insecta; Diptera; Brachycera; Muscomorpha;		
OC	Phylogeny: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
CC	Ephyroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID:7227;		
SN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRATIN-CANTON S.		
RX	STRATIN-CANTON S. Pubmed-663295.		
RT	Takahashi F., Endo S., Kohina T., Saigo K.;		
RT	"Regulation of cell-cell contacts in developing Drosophila eyes by		
RT	Dsrc41, a new, close relative of vertebrate c-src."		
RL	Genes Dev. 10:1645-1656(1996).		
DR	EMBL: D42125; BAA0705.1; -		
DR	HSSP: P00523; ISRL.		
DR	FLYBASE:FBgn004603; Src42A.		
DR	InterPro: IPR000980; -		
DR	InterPro: IPR001245; -		
DR	InterPro: IPR001452; -		
DR	PIfam: PF00017; SH2; 1		
DR	PIfam: PF00018; SH3; 1		
DR	PIfam: PF00069; PKinase; 1		
DR	PRINTS: PR00401; SH2KIN.		
DR	PRINTS: PR00452; SH3KIN.		
DR	PRINTS: PR00109; TYRKINASE.		
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1		
DR	PROSITE: PS00109; PROTEIN_KINASE_DOM; 1		
DR	PROSITE: PS00001; SH2; 1		
DR	PROSITE: PS00002; SH3; 1		
DR	SMART: SM00219; Tyrc1.1		
KN	ATP-binding; Transferase; Tyrosine-protein kinase.		

RA Zhao B., Xu Y.Y., Liu Y.Q., Wang X.Y., Lai B., Ye J., Song L.,
 RA Zhao Y., Cao H.Q., Zhao X.M., Gao Y., Zhang C.L., Zhang J., Liu L.S.,
 RA Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q., Yuan J.G., Liew C.C.,
 RA Zhao N.S., Hu J. 1999, to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF119814; AAC47945.1;
 SO SEQUENCE 1153 AA; 130800 MW; 327F6A675028DA59 CRC64;

Query Match 61.3% Score 38; DB 4; Length 1153;
 Best Local Similarity 58.3%; Pred. No. 94;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Y 2 RSSGSIASNYV 13
 :||||| :|||:
 Db 108 KNSGSIIDNYVR 119

RESULT 11
 ID 09P274 PRELIMINARY: PRT: 1265 AA.
 AC 09P274
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE KIAA1454 PROTEIN (FRAGMENT).
 GN KIAA1454
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=4027462; PubMed=10819331.
 RT "Prediction of the coding sequences of unidentified human
 RT genes XVII: the complete sequences of 100 new cDNA clones from brain
 RT which code for large proteins in vitro."
 RL DNA Res. 7:143-150(2000).
 DR EMBL: AB040887; BAA95978.1; -
 DR EMBL: AF000822;
 DR EMBL: F850018; ZINC_CINCR.CCH2; UNKNONN_1.
 PT NON-TER
 SO SEQUENCE 1265 AA; 142701 MW; 435912592B5862 CRC64;

Query Match 61.3% Score 38; DB 4; Length 1265;
 Best Local Similarity 58.3%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Y 2 RSSGSIASNYV 13
 :||||| :|||:
 Db 370 KNSGSIIDNYVR 381

RESULT 12
 ID 09A331 PRELIMINARY: PRT: 236 AA.
 AC 09A331
 DT 01-NOV-1999 (TEMBLrel. 12, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE PK01-61.
 OS Bacillus anthracis
 OC Bacteria; Firmicutes; Bacilli; Clostridium group;
 CC Bacillus/staphylococcus group; Bacillus.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=STERNE; CLOUD K., Hammon O., Hoffmaster A., Hill K.K., Keim P.,
 RA Kautler R.T., Lanke G., Romano S., Whittam T.S., Wontner D., Martinez Y.,
 RA

RA Ricke D.O., Svensson R., Jackson P.J.;
 RT "The sequence and organization of pXO1, the large Bacillus anthracis
 RT plasmid harboring the anthrax toxin genes."
 RT Plasmid 10:1-9(1989).
 DR EMBL: AF05404; AB023355.1; -
 KW Plasmid.
 SO SEQUENCE 236 AA; 27161 MW; BE140A755B87695 CRC64;

Query Match 59.7% Score 37; DB 2; Length 236;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Y 2 RSSGSIASNYV 13
 :||||| :|||:
 Db 25 KNSGSIIDNYVR 36

RESULT 13
 ID 091M00 PRELIMINARY: PRT: 140 AA.
 AC 091M00
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE F7H2.18 PROTEIN.
 GN F7H2.18
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV COLUMBIA.
 RA Liu S.X., Sakano H., Yu G., Egu P., Lee J., Lenz C., Pham P.,
 RA Toriumi M., Chan A., Chung M., Goldsmith A., Liu A., Smith A.,
 RA Vaysberg M., Atafifi H., Brooks S., Buehler E., Chao O., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shlim P., Southwick A., Davis R.M.,
 RA "The sequence of BAC F7H2 from Arabidopsis thaliana chromosome 1."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC034256; AAF82154.1; -
 DR InterPro: IP001680; -
 DR Pfam: PF00400; WD40.3;
 SO SEQUENCE 140 AA; 15056 MW; D2B0C857456D248C CRC64;

Query Match 58.1% Score 36; DB 10; Length 140;
 Best Local Similarity 88.9%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Y 1 TRSSGSIAS 9
 :||| :|||:
 Db 56 TRSSGSIAS 64

RESULT 14
 ID 054288 PRELIMINARY: PRT: 294 AA.
 AC 054288
 DT 01-JUN-1998 (TEMBLrel. 06, Created)
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
 DE 2-KETO-3-DEOXY GLUCONATE ALDOASE.
 OS Sulfolobus solfataricus.
 CC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JCM 1615;
 RA Kyd C.L., Danon M.J., Hough D.W., Reeve C.D.;

RL Submitted (FEH-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ224174; CA11866.1; -
 DR InterPro: IPR002220; -
 DR Pfam: PF00701; DDBPS; 1.
 DR ProDom: PD01859; -; 1.
 DR PROSITE: PS00001; -; 1.
 SQ SEQUENCE 294 AA; 3108 MM; D709A9ACF680EF CRC64;

Query Match

58.1%; Score 36; DB 1; Length 294;
 Best Local Similarity 58.3%; Pred. No. 52;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSCGSIASNY 12
 :|:::||||

DB 236 SIFGSIASNY 247

RESULT 15

OLHE5
 AC 09LHE5;

PRELIMINARY: PRT: 308 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DE MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (TRANSLOCASE OF OUTER

MEMBRANE 32 KDA SUBUNIT) (TOM40 PROTEIN).

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsia.

OX NCBI_TaxID=3702;

RN 11

RC STRAIN=CY COLIMBE1.

MDLINE=20363099; Pubmed-10907853.

RA Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.

RT Sequence features of the regions of 4,251,695 bp covered by ninety p1,

RT TAC and BAC clones";

RL DNA Res. 7:217-221(2000).

RP SEQUENCE OF 1-15; 21-42; 63-80; 207-219 AND 245-258

RA Werhann W., Nilmeyer A., Jaensch L., Krufc K., Schmitz U.K.,

RT "Purification and characterization of the preprotein translocase of

RT the outer mitochondrial membrane from Arabidopsis thaliana:

RT Identification of multiple forms of TOM40.";

CC Arabidopsis 7:209-216(2000).

CC -1- FUNCTION: ESSENTIAL FOR THE IMPORT OF PROTEIN PRECURSORS INTO THE

CC MITOCHONDRIA.

CC -1- SUBUNIT: FORMS PART OF MITOCHONDRIAL RECEPTOR COMPLEX.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

CC -1- OUTER MEMBRANE.

CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A

CC PROTEIN PROCESSING ARTIFACT.

DR EMBL: AP002050; B00345; AAT.SQ

KW Transport; Protein transport; Outer membrane; Mitochondrion;

KW Transmembrane.

FT INIT_MET 0

FT DOMAIN 1 70 INTERMEMBRANE (POTENTIAL) -

FT TRANSMEM 71 86 POTENTIAL.

FT CYTOPLASM 87 187 CYTOPLASMIC (POTENTIAL).

SQ SEQUENCE 308 AA; 34119 MM; A015F8796BAA720 CRC64;

Query Match

58.1%; Score 36; DB 10; Length 308;
 Best Local Similarity 54.5%; Pred. No. 54;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 SSCGSIASNY 13
 :|:::||||

DB 216 STCAVVMNYVO 226

Search completed: November 19, 2001, 08:25:03
 Job time: 741 sec

THIS PAGE BLANK (USPTO)

XX	MP1: 2001-080877/09.
XX	New genes encoding human platelet-expressed collagen receptor,
XX	glycoprotein VI, and its modulators, useful for preventing, treating
XX	platelet-mediated thrombotic disorders, thrombotic diseases and
XX	immunological disorders -
PX	Claim 32: Page 102; 227pp: English.
CC	The present sequence is given in a specification relating to an isolated
CC	nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC	and polypeptides (GPII _b /III _a , also called αIIbβ3). The GPII Polynucleotide
CC	sequence is set forth in SEQ ID NO. 1, and the amino acid sequence of the
CC	ribonzyme and antibodies are useful for preventing, treating and
CC	diagnosing disorders associated with aberrant expression or delivery of
CC	GVI. These disorders include bleeding disorders
CC	(e.g., thrombocytopenia), blood vessel injury, thrombotic disorders
CC	(e.g., thrombotic occlusion of the coronary arteries), haemorrhagic
CC	disorders, coronary artery and cerebral artery diseases (e.g., stroke and
CC	infarction), cardiovascular diseases (e.g., atherosclerosis) and myocardial
CC	infarction, liver disorders, preferably fatty liver disease, and prevent acute
CC	cardiac ischemia following angioplasty and metastatic cancers,
CC	especially of the colon and liver.
SQ	Sequence 13 AA:
XX	
Query Match	100.0%; Score 62; DB 22; Length 13;
Best Local Similarity	100.0%; Pctd. No. 2, 2c-05;
Matches 13: Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 TRSSGSINSNYQ 13 Db 1 crasgslnsnvyq 13
RESULT 2	
ID AAM16590	standard: Peptide: 13 AA.
AA16590:	
30-MOV-1997 (first entry)	
Anti-RSV F glycoprotein antibody RSVF2-5 light chain VL6 CDRL1.	
Respiratory syncytial virus; RSV: monoclonal antibody; CDR: complementarity determining region; pneumonia; bronchiolitis; diagnosis; Therapy; vaccine; RSVF2-5.	
Homo sapiens.	
M09710B46-A1.	
27-MAR-1997.	
18-SEP-1996: 96MO-US14937.	
18-SEP-1995: 95OUS-0003931.	
(INTRN.) INTRACEL CORP. (USSH) US DEPT HEALTH & HUMAN SERVICES.	
Chamock RM, Crowe JE, Gilmour PS, Murphy BR, Plakington GR; WPI: 1997-202621/18.	
Composition comprising respiratory syncytial virus antibody - useful for treatment or prophylaxis of active disease or infection	
Claim 9; Page 54; 71pp: English.	

[illegible]

XX XX
 PN MO9710846-A1.
 XX 27-MAR-1997.
 XX
 XX 18-SEP-1996; 96MO-US14937.
 PE
 PR 18-SEP-1995; 95US-0003931.
 XX
 XX (INTR-) INTRACEL CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Chanock RM, Crowe JE, Gilmour PS, Murphy BR, Pilkington GR;
 PI N-PSDB; AAT66557.
 DR
 XX
 PT Composition comprising respiratory syncytial virus antibody - useful
 for treatment or prophylaxis of active disease or infection
 PS Claim 10; Page 52-53; 71pp; English.
 XX
 XX This polypeptide sequence comprises the light chain V_{L6} region
 of a novel neutralising human monoclonal antibody to respiratory
 syncytial virus (RSV). The antibody, designated RSVF2-5 (ATCC
 65909), selectively binds to an RSV F glycoprotein epitope: CDNA
 encoding the RSVF2-5, the V_{H3} and light chain (the AAM16586-57)
 the RSVF2-5, the V_{H3} and light chain (the AAM16586-57)
 the peripheral blood lymphocytes of an HIV-1 infected donor. A
 claimed pharmaceutical preparation comprises a carrier and an
 antibody that includes the RSVF2-5 V_{H3} CDR3 (AAM16586) and which may
 also include the V_{H3} CDR2 (AAM16584) and/or CDR1 or the entire V_{L6}
 region (AAM16580), or is an Fd fragment and further includes the
 RSVF2-5 V_{L6} CDR3 (AAM16594), CDR2 (AAM16592), CDR1 (AAM16590) or a
 fragment thereof.
 CC carrier and a vector that includes a nucleotide sequence encoding
 the antibody. The preparations can be used for the treatment or
 CC prophylaxis of active RSV disease or infection (claimed), and may
 also be used for RSV detection. The antibody binds and neutralises
 CC antigenic subgroups A and B of RSV with high efficiency.
 XX
 XX Sequence 109 AA:
 S0
 Query Match 80.6%; Score 50; DB 18; Length 109;
 Best Local Similarity 76.9%; Pred. No. 0.046;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TRSSGSINATWQ 13
 DB 20 trsggrlssnyq 32
 ID AAM14785 standard; Protein; 109 AA.
 XX AAM14785.
 XX
 XX 20-JUN-1997 (first entry)
 DE Human monoclonal antibody RSVF2-5 light chain V_{L6}.
 KM Respiratory syncytial virus; RSV; monoclonal antibody; MAb;
 XX diagnosis; prophylaxis; immunotherapy; therapy; Fab; Fd.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..19
 FT Region /label= FR1
 FT Region 20..32
 FT Region /label= CDR1

ET /note= "Claim 9"
 FT Region
 ET 33..47
 FT /label= FR2
 FT Region
 ET /label= CDR2
 FT /note= "Claim 8"
 FT Region
 ET 55..88
 FT /label= FR3
 FT Region
 ET 89..98
 FT /label= CDR3
 FT /note= "Claim 7"
 FT Region
 ET 99..109
 FT /label= FR4
 XX
 XX MO9711177-A1.
 XX 27-MAR-1997.
 XX
 XX 18-SEP-1996; 96MO-US14944.
 PE
 PR 18-SEP-1995; 95US-0003931.
 XX
 XX (INTR-) INTRACEL CORP.
 PA Gilmour PS, Pilkington GR;
 PI NPI; 1997-202865/18.
 DR N-PSDB; AAT63418.
 XX
 PT Monoclonal antibody specific for respiratory syncytial virus - used
 for diagnosis and immuno-prophylaxis or immuno-therapy of RSV
 PT disease
 PS Claim 10; Page 49-50; 68pp; English.
 XX
 XX The light chain variable region (AAM14785) and heavy chain variable
 CC region (AAM14784) are provided of a novel, fully human monoclonal
 CC antibody (MAb), designated RSVF2-5, which selectively binds to
 CC the F glycoprotein of respiratory syncytial virus (RSV) and which
 CC neutralises RSV in vivo. To obtain RSVF2-5, a packaged phage
 CC library was prepd. from amplified heavy and light chain variable
 CC regions of a human monoclonal antibody (MAb) of group 1 on an
 CC HIV-1 infected donor. The phage library was panned with RSV
 CC proteins and isolated clones were sequenced. Isolated nucleic
 CC acids (AAT63417-18) can be used to produce novel polypeptides, esp.
 CC Fd or Fab fragments useful in the diagnosis of RSV disease, in the
 CC methods for detecting the presence of RSV in a sample, and in the
 CC immunoprophylaxis and immunotherapy of RSV disease.
 XX
 XX Sequence 109 AA:
 S0
 Query Match 80.6%; Score 50; DB 18; Length 109;
 Best Local Similarity 76.9%; Pred. No. 0.046;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TRSSGSINATWQ 13
 DB 20 trsggrlssnyq 32
 ID AAR23736 standard; Protein; 13 AA.
 XX AAR23736.
 XX
 XX 27-OCT-1992 (first entry)
 DE Ligand CDR(d).
 KM Complementarity determining region; heavy chain variable domain;
 XX antigen binding site.

XX OS Synthetic.
 XX PA N092061931-A.
 XX PD 16-APR-1992.
 XX PF 04-OCT-1991; 91MO-GB01726.
 XX PR 08-OCT-1990; 90GB-0021679.
 XX PA (GORMAN) GORMAN S D.
 XX PI Gorman SD, Routledge EG, Waldmann H;
 DR WPI: 1992-150879/18.
 DR N-PSDB: AAQ2340.
 CC Ligands and antibodies with binding affinity for CD3 antigen -
 CC for treatment of immunosuppression e.g. In graft rejection, and
 CC cancer, esp. lymphoid malignancies
 XX PS Disclosure: Page 4; 49pp; English.
 XX SQ
 CC The sequence given is a complementarity determining region (CDR)
 CC of the CDR(d). CDR's are found in the variable domains of light
 CC and heavy chain antibodies. They are the amino acid regions of the
 CC connectors between the four framework regions and act as
 CC It has been noted that there seem to be no characteristic features
 CC which distinguish human from mouse or rat CDR's and they are
 CC therefore immunologically identical. The CDR described is used in
 CC a ligand with a binding affinity for the human CD3 antigen within
 CC the framework regions of the heavy chain variable domain along with
 CC the CDR's described in AAQ23737 and AAQ23738.
 XX SQ
 SQ Sequence 13 AA:
 Query Match 62.9%; Score 39; DB 13; Length 13;
 Best Local Similarity 66.7%; Pred. No. 0.46;
 Matches 8; Conservative 2; Mismatches 0; Gaps 0;
 YY 1 TRSSGSIAINYY 12
 | |||:| |||
 Db 1 tlasgenlenny 12
 RESULT 6
 AAQ50108
 ID AAQ50108 standard: peptide, 13 AA.
 XX
 AC AAQ50108:
 XX
 DT 27-APR-1994 (first entry)
 XX
 DS CDR (d).
 XX
 KW Antibody: glycosylation: IgG; binding affinity: CD3; antigen:
 KW CDR; complementarity determining region; heavy chain; light chain;
 KW variable domain; immunosuppressant; T-cell; mitogenesis;
 KW cytokine; graft; rejection; cancer; proliferation.
 XX OS Synthetic.
 XX PA W09319196-A.
 XX PN W09319196-A.
 XX PD 30-SEP-1993.
 XX PF 21-OCT-1992; 92MO-GB01933.
 XX PR 24-MAR-1992; 92GB-0006422.
 XX PA (BOLT/) BOLT S L.

PA (CLARK/) CLARK M R.
 PA (GORMAN) GORMAN S D.
 PA (ROUT/) ROUTLEDGE E G.
 XX (WALD/) WALDMANN H.
 XX
 XX BOLT SL, Clark MR, Gorman SD, Routledge EG, Waldmann H;
 DR WPI: 1993-320762/40.
 DR
 XX
 PT Aglycosylated IgG antibody against human CD3 antigen - for
 PT preventing graft rejection and treating cancer, and does not
 PT induce T cell proliferation and cytokine prodn.
 XX PS Claim 3; Page 25; 41pp; English.
 XX SQ
 CC An aglycosylated IgG antibody having a binding affinity for the human
 CC CD3 antigen complex comprises at least one CDR selected from the amino
 CC acid sequences given in AAQ50105-P50110. The heavy and light chain
 CC variable domains of an aglycosylated antibody is given in AAQ41721-
 CC AAQ41722. The antibodies are useful as immunosuppressants. Unlike
 CC glycosylated antibodies, they do not induce T-cell mitogenesis nor
 CC do they cause high level release of cytokines.
 XX SQ
 SQ Sequence 13 AA:
 Query Match 62.9%; Score 39; DB 14; Length 13;
 Best Local Similarity 66.7%; Pred. No. 0.46;
 Matches 8; Conservative 2; Mismatches 0; Gaps 0;
 YY 1 TRSSGSIAINYY 12
 | |||:| |||
 Db 1 tlasgenlenny 12
 RESULT 7
 AAQ6804
 ID AAQ6804 standard: Peptide, 13 AA.
 XX
 AC AAQ6804:
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DS Amino acid sequence of CDR (d) of an anti-CD3 IgG antibody.
 XX
 KW Complementarity determining region: CDR; rat; immunoglobulin G; IgG;
 KW CD3 antigen complex; chimeric antibody; immunosuppression;
 KW CD3 antigen-T-cell receptor complex; graft rejection; cancer.
 XX OS Rattus sp.
 XX PA W0200005268-A1.
 XX PN W0200005268-A1.
 XX PD 03-FEB-2000.
 XX PF 21-JUL-1999; 99MO-GB02380.
 XX PR 21-JUL-1998; 98GB-0015909.
 XX PA (BRGT-) BRG INT LTD.
 XX PI Waldmann H, Frewin M;
 DR WPI: 2000-182655/16.
 DR N-PSDB: AAQ60593.
 XX New humanized anti-CD3 antibodies, used for treating cancer or for
 XX immunosuppression and preventing graft rejection -
 XX PS Claim 1; Page 38; 56pp; English.
 XX SQ
 CC AAQ6801-06 represent complementarity determining regions (CDRs) of a
 CC rat immunoglobulin G (IgG) antibody which is specific for the CD3

CC antigen complex. The CDR regions are used to produce chimeric
 CC human/rodent anti-CD3 antibodies, which have a rodent CD3 light chain
 CC variable region and a human heavy chain variable region. The anti-CD3
 CC antibodies are used to treat human T-cell leukemia. One of the
 CC CD3 antigen-T-cell receptor (TCR) complex. They can be used for
 CC immunosuppression, particularly for the control of graft rejection.
 CC The antibodies can also enhance or re-direct T-cell responses to
 CC antigens. They can be used in the treatment of cancer.
 CC
 SQ Sequence 13 AA:
 62.9%: Score 39; DB 21; Length 13;
 Query Match Best Local Similarity 66.7%: Pred. No. 0.46;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNV 12
 1 11111:111
 DB 1 t13sgslennvy 12
 RESULT 8
 AAY68807
 ID AAY68807 standard; Protein; 111 AA.
 AC AAY68807:
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DE A light chain variable region of a rat anti-CD3 IgG antibody.
 XX
 KM CD3 antigen complex; chimeric antibody; immunosuppression; light chain;
 XX CD3 antigen-T-cell receptor complex; graft rejection; cancer.
 KM
 XX Rattus sp.
 XX
 PN MO200005268-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99MO-C802380.
 XX
 PR 21-JUL-1998; 98GB-0015909.
 XX
 XX (BTCL-) BTG INT LTD.
 PA
 XX Waldmann H, Frewin M;
 PI
 XX NPL: 2000-182655/16.
 XX
 DR NPSDB; AAY68807.
 XX
 PT New humanized anti-CD3 antibodies, used for treating cancer or for
 XX immunosuppression and preventing graft rejection
 PS
 XX Claim 5: Page 40-41; 56pp; English.
 XX
 CC The present sequence represents the light chain variable region of a rat
 CC human/rodent anti-CD3 antibody, which has a rodent CD3 light chain
 CC complex. The light chain variable regions is used to produce chimeric
 CC human/rodent anti-CD3 antibodies, which have a rodent CD3 light chain
 CC variable region and a human heavy chain variable region. The anti-CD3
 CC antibodies can render T-cells non-functional by antibody blockade of
 CC the CD3 antigen-T-cell receptor (TCR) complex. They can be used for
 CC immunosuppression, particularly for the control of graft rejection.
 CC The antibodies can also enhance or re-direct T-cell responses to
 CC antigens. They can be used in the treatment of cancer.
 CC
 SQ Sequence 111 AA:
 62.9%: Score 39; DB 21; Length 111;
 Query Match Best Local Similarity 66.7%: Pred. No. 5;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNV 12
 11111:111
 DB 23 t13sgslennvy 34
 RESULT 9
 AAR23772
 ID AAR23772 standard; Protein; 128 AA.
 AC AAR23772:
 XX
 DT 27-OCT-1992 (first entry)
 XX
 DE Recombinant light chain variable domain (6).
 XX
 KM Complementarity determining region; light chain variable domain;
 XX antigen binding site; ligand; framework region; cancer; transplant.
 KM
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 23..35
 FT Label- CDR(d)
 FT Region 51..57
 FT Label- CDR(e)
 FT Region 61-68
 FT Label- CDR(e)
 XX
 PN MO9206193-A.
 XX
 PD 16-APR-1992.
 XX
 PF 04-OCT-1991; 91MO-C801726.
 XX
 PR 05-OCT-1990; 90GB-0021679.
 XX
 XX (GORM/) GORMAN S D.
 PA
 XX Gorman SD, Routledge RC, Waldmann H;
 PI
 XX NPL: 1992-150879/18.
 XX
 PT Ligands and antibodies with binding affinity for CD3 antigen -
 XX for treatment of immunosuppression e.g. in graft rejection, and
 PT cancer, esp. lymphoid malignancies
 PS
 XX Claim 7: Page 31; 49pp; English.
 XX
 CC The sequence given is a recombinant human light chain variable
 CC domain, ligand containing the complementarity determining region
 CC (CDR) given in AAR23736 and AAR23737. CDR's are found in the variable
 CC domains of light and heavy chains which form the antigen binding site,
 CC and act as connectors between the four framework regions.
 CC It has been noted that there seem to be no characteristic features
 CC which distinguish human from mouse or rat CDR's and they are
 CC therefore immunologically identical to those of immunological
 CC response caused by the synthetic CDR's the light chain can be considered
 CC to be humanised. This ligand can be are used to manufacture medicaments
 CC for use in immunosuppression esp. in patients with cancer or transplant
 CC recipients.
 CC
 SQ Sequence 128 AA:
 62.9%: Score 39; DB 13; Length 128;
 Query Match Best Local Similarity 66.7%: Pred. No. 6.5;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNV 12
 23 t13sgslennvy 34

	RESULT	10
ID	AAR23778 standard; Protein:	128 AA.
AC	MAR23778;	
DQ	27-OCT-1992 ((first entry))	
XX	Recombinant Light chain variable domain (11).	
DE	Complementarily determining region: Light chain variable domain:	
KM	Antigen binding site: Ligand: framework region; cancer; transplant.	
XX	Synthetic.	
OS		
FX	Key	Location/Ovalifiers
FH	Region	21..25 CDR(e)
FT	Region	45..67 CDR(e)
FT	/Label= CDR(d)	92..98
FT	Region	/Label= CDR(e)
PX	W09206193.A.	
PN	16-APR-1992.	
PX	04-OCT-1991:	91MO-GRI01726.
PF	05-OCT-1990:	90GB-0021679.
PR	(GORUK) GORMAN S D.	
PA	Gorman SD, Roulledge BC, Waldmann H:	
XI	WPJ: 1992-150879/18.	
DT	Ligands and antibodies with binding affinity for CD3 antigen -	
PT	for treatment of immunosuppression e.g. In graft rejection, and	
PT	cancer, esp. lymphoid malignancies	
XX	Claim 7: Page 31: 49pp: English.	
PS	The sequence given is a recombinant human light chain variable	
XX	region ligand containing the complementarily determining region	
CC	(CDP) amino acid residues 21 through 98. The CDR's are found in the	
CC	variable domains of light and heavy chains of antibody molecules.	
CC	binding sites, and act as connectors between the four features.	
CC	It has been noted that there seem to be no characteristic features	
CC	which distinguish human from mouse or rat CDR's and they are	
CC	therefore immunologically identical. This ligand has binding affinity	
CC	response caused by the synthetic CDR's the ligand can be considered	
CC	to be humanized. This ligand can be used to manufacture medicaments	
CC	in immunosuppression esp. in patients with cancer or transplant	
CC	recipients.	
SO	Sequence	128 AA:
Query Match	62.9%; Score 39; DB 13; Length 128;	
Best Local Similarity	66.7%; Pred.No. 6.5;	
Matches	8: Conservative 2: Mismatches 2: Indels 0: Gaps 0:	
OY	1 TRASSGSIASNYV 12	
I	IIIVLILIVLLVV	
Dd	45 Ilaaglamyvv 56	
RESULT	11	
AAR23814		

ID	AA023014	standard; Protein; 128 AA.
XX	AA023014:	
XX	27-OCT-1992	(first entry)
XX	Recombinant light chain variable domain (13).	
XX	Complementarity determining region; light chain variable domain;	
XX	antigen binding site; ligand: framework region; cancer: transplant.	
XX	Synthetic.	
XX	Key	Location/Qualifiers
XX	Region	23..29
XX	Region	/label= CDR(e)
XX	Region	45..51
XX	Region	/label= CDR(e)
XX	Region	86..98
XX	Region	/label= CDR(d)
XX	MO0206193-A.	
XX	16-APR-1992.	
XX	04-OCT-1991:	91WO-GB01726.
XX	05-OCT-1990:	90GB-0021679.
XX	(GORMY) GORMAN S. D.	
XX	Gorman SD, Routledge EG, Waldmann H;	
XX	MP1: 1992-150879/18.	
XX	Ligands and antibodies with binding affinity for CD3 antigen -	
XX	for treatment of immunosuppression e.g. in graft rejection, and	
XX	cancer, esp. lymphoid malignancies	
XX	Claim 7: Page 31; 49pp: English.	
XX	The sequence given is a recombinant human light chain variable	
XX	domain ligand containing the complementarity determining region	
XX	CDR1 and CDR2. CDR3's are found in the	
XX	variable domains of light and heavy chains for the antigen	
XX	binding site, and act as connectors between the four framework regions.	
XX	It has been noted that there seem to be no characteristic features	
XX	which distinguish human from mouse or rat CDR's and they are	
XX	therefore immunologically identical. This ligand has binding affinity	
XX	for the human CD3 antigen and due to the lack of immunological	
XX	response caused by the synthetic CDR's the ligand can be considered to	
XX	be used in this ligand can be used to manufacture medicaments	
XX	for use in immunosuppression esp. in patients with cancer or transplant	
XX	recipients	
XX	Sequence 128 AA:	
XX	Sequence 128 AA:	
XX	Query Match	62 5% Score 39; DB 13; Length 128;
XX	BLAST Local	66.7% Prev. NO. 6.5;
XX	Matches 8; Conservative 2; Mismatches 2;	Indels 0; Gaps 0;
XX	1 TRSSGSLSINMY 12	:
XX	Db 86 tlasglenmy 97	
XX	RESUME 12	
XX	AA023740	standard; Protein; 130 AA.
XX	AA023740:	
XX	AA023740:	

XX	Complementarity determining region: light chain variable domain:
KX	antigen binding site; ligand: framework region; cancer: transplant.
XX	Synthetic.
OS	
XX	Key
PH	Region
FT	23..53
FT	/Label= CDR(d)
FT	51..59
FT	/Label= CDR(f)
FT	93..100
FT	/Label= CDR(e)
XX	
XX	W09206193.A.
XX	16-APR-1992.
PD	
PD	04-OCT-1991: 91WO-0801726.
XX	
XX	05-OCT-1990: 90GB-0021679.
XX	
XX	(GORMA/) GORMAN S D.
XX	
PI	Gorman SD, Roulledge BE, Waldmann H:
XX	WPI: 1992-150879/18.
DR	
XX	
XX	Ligands and antibodies with binding affinity for CD3 antigen -
PT	for treatment of immunosuppression e.g. in graft rejection, and
PT	cancer, esp. lymphoid malignancies
PS	Claim 7: Page 31: 49pp. English.
XX	
XX	The sequence given is a recombinant human light chain variable
CC	domain ligand containing the complementarity determining region
CC	(CDR) given in AAR23736, AAR3737 and AAR3738. CDR's are found in the
CC	variable domains of light and heavy chains which form the antigen
CC	binding site, and act as connectors between the four framework regions.
CC	It should be noted that the amino acid sequences of the CDR's are
CC	which distinguish human from mouse or rat CDR's and they are
CC	therefore immunologically identical. This ligand has binding affinity
CC	for the human CD3 antigen and due to the lack of immunological
CC	response caused by the synthetic CDR's the ligand can be considered to
CC	be humanised. This ligand can be are used to manufacture medicaments
CC	for use in immunosuppression esp. in patients with cancer or transplant
XX	recipients.
XX	
XX	Sequence 130 AA:
SO	
XX	
XX	Query Match 62.9%; Score 39; DB 13; Length 130;
XX	Best Local Similarity 66.7%; Pred. No. 6.6;
XX	Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY	1 TRSSGSINRY 12
DB	11111:1111
DB	23 t1ssgslnny 34
XX	
XX	RESULT 14
XX	AAR23736
XX	100 AAR23779 standard: Protein; 130 AA.
XX	AAR23779;
XX	
XX	27-OCT-1992 (first entry)
XX	
XX	Recombinant light chain variable domain (12).
XX	
XX	Complementarity determining region: light chain variable domain:
KX	antigen binding site; ligand: framework region; cancer: transplant.

THIS PAGE BLANK (USPTO)

RESULT 2
 US-09-610-118-64
 ? SEQUENCE 2358, Application US/09610118
 ? GENERAL INFORMATION:
 ? APPLICANT: Busfield, S.
 ? APPLICANT: Villaveil, J.
 ? APPLICANT: Jandrot-Perrus, M.
 ? APPLICANT: Valchenker, W.
 ? APPLICANT: Gull, D.
 ? APPLICANT: M. Kishelyev, G.
 ? TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
 ? FILE REFERENCE: 7853-211
 ? CURRENT FILING DATE: 2000-06-30
 ? PRIOR APPLICATION NUMBER: US/09/503,397
 ? PRIOR FILING DATE: 2/14/00
 ? PRIOR APPLICATION NUMBER: 09/454,824
 ? PRIOR FILING DATE: 12/6/99
 ? PRIOR APPLICATION NUMBER: 09/345,468
 ? PRIOR FILING DATE: 6/30/99
 ? NUMBER OF SEQ ID NOS: 72
 ? SOFTWARE: FASTSEQ for Windows Version 3.0
 ? SEQ ID NO 64
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 US-09-610-118-64

Query Match
 Best Local Similarity 100.0%; Score 62; DB 20; Length 13;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNYVO 13
 DB 1 TRSSGSIASNYVO 13
 RESULT 3
 US-09-832-312-64
 ? SEQUENCE 64, Application US/09832312
 ? GENERAL INFORMATION:
 ? APPLICANT: Busfield et al.
 ? TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
 ? FILE REFERENCE: 7853-234
 ? CURRENT FILING DATE: 2000-06-30
 ? PRIOR APPLICATION NUMBER: US/09/832,312
 ? PRIOR FILING DATE: 2000-06-30
 ? PRIOR APPLICATION NUMBER: 09/503,387
 ? PRIOR FILING DATE: 2000-02-14
 ? PRIOR APPLICATION NUMBER: 09/454,824
 ? PRIOR FILING DATE: 12/6/99
 ? PRIOR APPLICATION NUMBER: 09/345,468
 ? PRIOR FILING DATE: 1999-06-30
 ? NUMBER OF SEQ ID NOS: 78
 ? SOFTWARE: FASTSEQ for Windows Version 3.0
 ? SEQ ID NO 64
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 US-09-832-312-64

Query Match
 Best Local Similarity 100.0%; Score 62; DB 22; Length 13;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNYVO 13
 DB 1 TRSSGSIASNYVO 13

RESULT 4
 US-60-195-053-2358
 ? SEQUENCE 2358, Application US/60195053
 ? GENERAL INFORMATION:
 ? APPLICANT: Bonazzi, Yvlen
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 ? FILE REFERENCE: C1000427
 ? CURRENT FILING DATE: 2000-04-06
 ? PRIOR APPLICATION NUMBER: US/60/195,053
 ? PRIOR FILING DATE: 2000-04-06
 ? NUMBER OF SEQ ID NOS: 2836
 ? SOFTWARE: FASTSEQ for Windows Version 4.0
 ? SEQ ID NO 2358
 ? LENGTH: 88
 ? TYPE: PRT
 ? ORGANISM: HUMAN
 US-60-195-053-2358

Query Match
 Best Local Similarity 100.0%; Score 62; DB 24; Length 88;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNYVO 13
 DB 45 TRSSGSIASNYVO 57

RESULT 5
 US-60-195-053-2359
 ? SEQUENCE 2359, Application US/60195053
 ? GENERAL INFORMATION:
 ? APPLICANT: Bonazzi, Yvlen
 ? TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ? TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 ? FILE REFERENCE: C1000427
 ? CURRENT FILING DATE: 2000-04-06
 ? PRIOR APPLICATION NUMBER: US/60/195,053
 ? PRIOR FILING DATE: 2000-04-06
 ? NUMBER OF SEQ ID NOS: 2836
 ? SOFTWARE: FASTSEQ for Windows Version 4.0
 ? SEQ ID NO 2359
 ? LENGTH: 94
 ? TYPE: PRT
 ? ORGANISM: HUMAN
 US-60-195-053-2359

Query Match
 Best Local Similarity 100.0%; Score 62; DB 24; Length 94;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNYVO 13
 DB 42 TRSSGSIASNYVO 54

RESULT 6
 US-60-196-710-4905
 ? SEQUENCE 4905, Application US/60196710
 ? GENERAL INFORMATION:
 ? APPLICANT: Bonazzi, Yvlen
 ? TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
 ? TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS, AND
 ? FILE REFERENCE: C1000450
 ? CURRENT FILING DATE: 2000-04-13
 ? NUMBER OF SEQ ID NOS: 7166
 ? SOFTWARE: FASTSEQ for Windows Version 4.0


```

; SEQ ID NO 4905
; LENGTH: 100
; DB: US01
; ORGANISM: HUMAN
US-60-196-710-4905

```

```

Query Match
Best Local Similarity 100.0%; Score 62; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TRSSGSIASNYVO 13
Db 45 TRSSGSIASNYVO 57

```

```

RESULT 7
US-60-196-718-4971
; SEQUENCE: 196-718-4971
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: C1000456
; CURRENT APPLICATION NUMBER: US/60/196-718
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 2494-04-13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4971
; LENGTH: 100
; TYPE: PRT
; ORGANISM: HUMAN
US-60-196-718-4971

```

```

Query Match
Best Local Similarity 100.0%; Score 62; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TRSSGSIASNYVO 13
Db 45 TRSSGSIASNYVO 57

```

```

RESULT 8
PCT-US00-26524B-6775
; Sequence 6775, Application PC/TUS0026524B
; GENERAL INFORMATION:
; APPLICANT: Birge et. al.
; TITLE OF INVENTION: Protein and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: P00050CT
; CURRENT APPLICATION NUMBER: PCT/US00/26524B
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR FILING DATE: 1999-11-03
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6775
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: SITE
; LOCATION: 1149
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US00-26524B-6775

```

```

Query Match
Best Local Similarity 100.0%; Score 62; DB 1; Length 161;
Best Local Similarity 100.0%; Pred. No. 0.0028;

```

```

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TRSSGSIASNYVO 13
Db 44 TRSSGSIASNYVO 56

```

```

RESULT 9
PCT-US01-19110-1234
; Sequence 1234, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Immunogen Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bvys
; FILE REFERENCE: P523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3259
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1234
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1234

```

```

Query Match
Best Local Similarity 92.3%; Score 56; DB 1; Length 258;
Best Local Similarity 92.3%; Pred. No. 0.0066;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TRSSGSIASNYVO 13
Db 170 TRSSGSIASNYVO 162

```

```

RESULT 10
US-09-880-748-1234
; Sequence 1234, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bvys
; FILE REFERENCE: P523PCT
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1234
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1234

```

```

Query Match
Best Local Similarity 90.3%; Score 56; DB 22; Length 258;

```

Best Local Similarity 92.3%; Pred. No. 0.066;
Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TRSSGSIASNYVO 13
DB 170 TRSSGSIASNYVO 182

RESULT 11
US-09-043-522A-11
Sequence 11, Application US/09043522A
GENERAL INFORMATION:
APPLICANT: Intracel Corporation
APPLICANT: Gilmour, Glenn
APPLICANT: Gilmour, Glenn
TITLE OF INVENTION: Neutralizing Monoclonal Antibodies to Respiratory Syncytial Virus
FILE REFERENCE: 58138-083
CURRENT APPLICATION NUMBER: US/09/043,522A
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 13
TYPE: PRP
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: region
US-09-043-522A-11 (1)-(13)

Query Match

88.7%; Score 55; DB 14; Length 13;

Best Local Similarity 84.6%; Pred. No. 0.0032;
Matches 11: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 TRSSGSIASNYVO 13
DB 1 TRAGSSIASNYVO 13

RESULT 12
US-09-043-530-11
Sequence 11, Application US/09043530
GENERAL INFORMATION:
APPLICANT: Intracel Corporation
APPLICANT: Pilkington, Glenn
APPLICANT: Gilmour, Glenn
APPLICANT: Chanock, Robert
APPLICANT: Crose, James
APPLICANT: Chanock, Robert
TITLE OF INVENTION: Neutralizing Monoclonal Antibodies to Respiratory Syncytial Virus
FILE REFERENCE: 58138-084
CURRENT APPLICATION NUMBER: US/09/043,530
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 13
TYPE: PRP
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: region
US-09-043-530-11 (1)-(13)

Query Match

88.7%; Score 55; DB 14; Length 13;

Best Local Similarity 84.6%; Pred. No. 0.0032;
Matches 11: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 TRSSGSIASNYVO 13
DB 1 TRAGSSIASNYVO 13

RESULT 13
US-60-163-062-790
Sequence 790, Application US/60163062
GENERAL INFORMATION:
APPLICANT: Bioreze, Vivien
APPLICANT: Bioreze, Vivien
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID SEQUENCES ENCODING HUMAN KINASE PROTEINS AND USES
TITLE OF INVENTION: THEROP
FILE REFERENCE: C1000134
CURRENT APPLICATION NUMBER: US/60/163,062
CURRENT FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 1302
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 790
LENGTH: 79
TYPE: PRP
ORGANISM: Human
US-60-163-062-790

Query Match

88.7%; Score 55; DB 24; Length 79;

Best Local Similarity 92.3%; Pred. No. 0.026;
Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TRSSGSIASNYVO 13
DB 9 TGSSGSIASNYVO 21

RESULT 14
US-60-163-062-948
Sequence 948, Application US/60163062
GENERAL INFORMATION:
APPLICANT: Bioreze, Vivien
APPLICANT: Bioreze, Vivien
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID SEQUENCES ENCODING HUMAN KINASE PROTEINS AND USES
TITLE OF INVENTION: THEROP
FILE REFERENCE: C1000134
CURRENT APPLICATION NUMBER: US/60/163,062
CURRENT FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 1302
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 948
LENGTH: 79
TYPE: PRP
ORGANISM: Human
US-60-163-062-948

Query Match

88.7%; Score 55; DB 24; Length 79;

Best Local Similarity 92.3%; Pred. No. 0.026;
Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TRSSGSIASNYVO 13
DB 9 TGSSGSIASNYVO 21

RESULT 15
US-60-163-123-1181
Sequence 1181, Application US/60163123
GENERAL INFORMATION:
APPLICANT: Bioreze, Vivien
APPLICANT: Bioreze, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, NUCLEIC ACID SEQUENCES ENCODING HUMAN SECRETED PROTEINS AND USES
TITLE OF INVENTION: THEROP
FILE REFERENCE: C1000137
CURRENT APPLICATION NUMBER: US/60/163,123
CURRENT FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 1986
SOFTWARE: FASTSEQ for Windows Version 4.0

```

; SEQ ID NO 1181
; LENGTH: 94
; TYPE: prt
; ORGANISM: Human
US-60-163-123-1181

```

```

Query Match: 88 74; Score 55; DB 24; Length 96;
Best Local Similarity 92.38;
Pred. No. 0.032; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;
QY 1 TRSSSLASNYQ 13
| | | | | | | | | |
DB 25 TRSSSLASNYQ 37

```

Search completed: November 19, 2001, 08:23:16
Job time: 729 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: November 19, 2001, 08:23:31 ; Search time 11.44 Seconds

(without alignments)
6.053 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSGSIASNWYQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 25229 segs, 5326477 residues

Total number of hits satisfying chosen parameters: 25229

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2-6/p/odata1/paa/PC1_NEW.COMB.pep:*
2: /cgn2-6/p/odata1/paa/US06_NEW.COMB.pep:*
3: /cgn2-6/p/odata1/paa/US07_NEW.COMB.pep:*
4: /cgn2-6/p/odata1/paa/US08_NEW.COMB.pep:*
5: /cgn2-6/p/odata1/paa/US09_NEW.COMB.pep:*
6: /cgn2-6/p/odata1/paa/US06_NEW.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	55	88.7	13	5	US-09-972-656-2
2	55	88.7	13	5	US-09-972-656-108
3	55	88.7	13	5	US-09-972-656-108
4	54	87.1	21	5	US-09-972-656-90
5	50	80.6	13	5	US-09-972-656-130
6	50	80.6	103	5	US-09-972-656-130
7	50	80.6	217	5	US-09-972-656-88
8	47	75.8	13	5	US-09-972-656-9
9	47	75.8	13	5	US-09-972-656-102
10	47	75.8	13	5	US-09-972-656-102
11	47	75.8	13	5	US-09-972-656-102
12	47	75.8	13	5	US-09-972-656-102
13	47	75.8	13	5	US-09-972-656-102
14	47	75.8	13	5	US-09-972-656-102
15	47	75.8	13	5	US-09-972-656-102
16	47	75.8	13	5	US-09-972-656-102
17	47	75.8	13	5	US-09-972-656-102
18	47	75.8	13	5	US-09-972-656-102
19	47	75.8	13	5	US-09-972-656-102
20	47	75.8	13	5	US-09-972-656-102
21	47	75.8	13	5	US-09-972-656-102
22	47	75.8	13	5	US-09-972-656-102
23	47	75.8	13	5	US-09-972-656-102
24	47	75.8	13	5	US-09-972-656-102
25	47	75.8	13	5	US-09-972-656-102
26	47	75.8	13	5	US-09-972-656-102
27	47	75.8	13	5	US-09-972-656-102

ALIGNMENTS

28	32	51.6	316	5	US-09-957-944-8	Sequence 8, App1
29	32	51.6	316	5	US-09-328-393-19	Sequence 19, App1
30	32	51.6	316	5	US-09-328-393-19	Sequence 6, App1
31	32	51.6	316	5	US-09-957-944-6	Sequence 2, App1
32	31	50.0	317	5	US-09-787-126-2	Sequence 6, App1
33	31	50.0	317	5	US-09-957-944-6	Sequence 13, App1
34	31	50.0	317	5	US-09-877-633-13	Sequence 14, App1
35	31	50.0	317	5	US-09-877-633-13	Sequence 13, App1
36	31	50.0	317	5	US-09-877-633-13	Sequence 13, App1
37	31	50.0	317	5	US-09-877-633-13	Sequence 13, App1
38	31	50.0	317	5	US-09-877-633-13	Sequence 13, App1
39	31	50.0	317	5	US-09-877-633-13	Sequence 13, App1
40	30	48.4	316	5	US-09-815-242-13317	Sequence 13, App1
41	30	48.4	316	5	US-09-815-242-13317	Sequence 13, App1
42	30	48.4	316	5	US-09-815-242-13317	Sequence 13, App1
43	30	48.4	316	5	US-09-815-242-13317	Sequence 13, App1
44	30	48.4	316	5	US-09-815-242-13317	Sequence 13, App1
45	30	48.4	316	5	US-09-815-242-13317	Sequence 13, App1

```

RESULT 1
US-09-972-656-2
Sequence 2, Application US/09972656
APPLICANT: Deshpande, Rajendra
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972, 656
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-656-2

Query Match      88.7% Score 55: DB 5: Length 13:
Best Local Similarity 92.3% Pred. No. 6.4e-05:
Matches 11: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY      1 TRSSGSIASNWYQ 13
DB      1 TRSSGSIASNWYQ 13

RESULT 2
US-09-972-656-108
Sequence 108, Application US/09972656
APPLICANT: Deshpande, Rajendra
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972, 656
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 108
LENGTH: 216
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-656-108

Query Match      88.7% Score 55: DB 5: Length 216:

```

Best Local Similarity 92.3%; Pred. No. 0.0012;
 Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TRSSGSINNYQ 13
 1 | | | | | | | | | | | | | |
 Db 23 TGSSEGSINNYQ 35

RESULT 3
 US-09-972-656-3
 ; GENERAL INFORMATION:
 ; APPLICANT: Deshpande, Rajendra
 ; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
 ; FILE REFERENCE: A-799
 ; CURRENT APPLICATION NUMBER: US/09/972.656
 ; CURRENT FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-972-656-3

Query Match
 Best Local Similarity 92.3%; Pred. No. 9.8e-05; Length 13;
 Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSINNYQ 13
 1 | | | | | | | | | | | | | |
 Db 1 TRSSGSINNYQ 13

RESULT 4
 US-09-972-656-90
 ; Sequence 90, Application US/09972656
 ; GENERAL INFORMATION:
 ; APPLICANT: Deshpande, Rajendra
 ; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
 ; FILE REFERENCE: A-799
 ; CURRENT APPLICATION NUMBER: US/09/972.656
 ; CURRENT FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 90
 ; LENGTH: 216
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-972-656-90

Query Match
 Best Local Similarity 92.3%; Pred. No. 0.0018;
 Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSINNYQ 13
 1 | | | | | | | | | | | | | |
 Db 23 TRSSGSINNYQ 35

RESULT 5
 US-09-972-656-1
 ; Sequence 1, Application US/09972656
 ; GENERAL INFORMATION:
 ; APPLICANT: Deshpande, Rajendra
 ; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

; TITLE OF INVENTION: Neutralizing Activity
 ; FILE REFERENCE: A-799
 ; CURRENT APPLICATION NUMBER: US/09/972.656
 ; CURRENT FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-972-656-1

Query Match
 Best Local Similarity 84.6%; Pred. No. 0.00052; Length 13;
 Matches 11: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRSSGSINNYQ 13
 1 | | | | | | | | | | | | | |
 Db 1 TGSSEGSINNYQ 13

RESULT 6
 US-09-972-656-130
 ; Sequence 130, Application US/09972656
 ; GENERAL INFORMATION:
 ; APPLICANT: Deshpande, Rajendra
 ; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
 ; FILE REFERENCE: A-799
 ; CURRENT APPLICATION NUMBER: US/09/972.656
 ; CURRENT FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 130
 ; LENGTH: 103
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-972-656-130

; FEATURE:
 ; NAME/KEY: MISC.
 ; LOCATION: (7)..(7)
 ; NAME/KEY: UNIDENTIFIED
 ; LOCATION: (33)..(33)
 ; OTHER INFORMATION: UNIDENTIFIED
 ; NAME/KEY: MISC.
 ; LOCATION: (34)..(34)
 ; OTHER INFORMATION: UNIDENTIFIED
 ; NAME/KEY: MISC.
 ; LOCATION: (35)
 ; OTHER INFORMATION: UNIDENTIFIED
 ; NAME/KEY: MISC.
 ; LOCATION: (36)..(36)
 ; OTHER INFORMATION: UNIDENTIFIED
 US-09-972-656-130

Query Match
 Best Local Similarity 76.5%; Pred. No. 0.0045; Length 103;
 Matches 13: Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 TRSSGSIN--NYQ 13
 1 | | | | | | | | | | | | | |
 Db 24 TRSSGSINXXXXNYQ 40

RESULT 7
 US-09-972-656-88
 ; Sequence 88, Application US/09972656
 ; GENERAL INFORMATION:
 ; APPLICANT: Deshpande, Rajendra

```

? TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
? FILE OF INVENTION: 109
? CURRENT APPLICATION NUMBER: US/09/972.656
? CURRENT FILING DATE: 2001-10-05
? NUMBER OF SEQ ID NOS: 135
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 88
? LENGTH: 217
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-972-656-98

```

```

Query Match
Best Local Similarity 80.6%; Score 50; DB 5; Length 217;
Matches 11: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TRSSGSINMYV 13
1 |1111111111111111
DB 23 TGSSGSINMYV 35

```

```

RESULT 8
US-09-972-656-9
? SEQUENCE: Application US/09972656
? GENERAL INFORMATION:
? APPLICANT: Deshpande, Rajendra
? APPLICANT: Tsai, Mei-Mei
? TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
? FILE OF INVENTION: Neutralizing Activity
? FILE REFERENCE: A-799
? CURRENT APPLICATION NUMBER: US/09/972.656
? CURRENT FILING DATE: 2001-10-05
? NUMBER OF SEQ ID NOS: 135
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 9
? LENGTH: 13
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-972-656-9

```

```

Query Match
Best Local Similarity 75.8%; Score 47; DB 5; Length 13;
Matches 10: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TRSSGSINMYV 12
1 |1111111111111111
DB 1 TGSSGSINMYV 12

```

```

RESULT 9
US-09-972-656-102
? SEQUENCE: Application US/09972656
? GENERAL INFORMATION:
? APPLICANT: Deshpande, Rajendra
? APPLICANT: Tsai, Mei-Mei
? TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
? FILE OF INVENTION: Neutralizing Activity
? FILE REFERENCE: A-799
? CURRENT APPLICATION NUMBER: US/09/972.656
? CURRENT FILING DATE: 2001-10-05
? NUMBER OF SEQ ID NOS: 135
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 102
? LENGTH: 218
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-972-656-102

```

```

Query Match 75.8%; Score 47; DB 5; Length 218;

```

```

Best Local Similarity 83.3%; Pred. No. 0.035;
Matches 10: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TRSSGSINMYV 12
1 |1111111111111111
DB 23 TGSSGSINMYV 34

```

```

RESULT 10
US-09-975-901-18
? SEQUENCE: Application US/09975901
? GENERAL INFORMATION:
? APPLICANT: Davis, George E.
? APPLICANT: Bell, Scott E.
? TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING CMG PROTEINS, CMG PROTEINS, AN
? FILE OF INVENTION: FOR THEIR USE
? FILE REFERENCE: 12740.0245.NP0500
? CURRENT APPLICATION NUMBER: US/09/975.901
? CURRENT FILING DATE: 2001-10-12
? PRIOR APPLICATION NUMBER: US 6,023,972
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 18
? LENGTH: 174
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-975-901-18

```

```

Query Match
Best Local Similarity 56.5%; Score 35; DB 5; Length 174;
Matches 5: Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 4 SCSIASNYV 13
1 |1111111111111111
DB 19 SCSVANNWIE 28

```

```

RESULT 11
US-09-975-901-5
? SEQUENCE: Application US/09975901
? GENERAL INFORMATION:
? APPLICANT: Davis, George E.
? APPLICANT: Bell, Scott E.
? TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING CMG PROTEINS, CMG PROTEINS, AN
? FILE OF INVENTION: FOR THEIR USE
? FILE REFERENCE: 12740.0245.NP0500
? CURRENT APPLICATION NUMBER: US/09/975.901
? CURRENT FILING DATE: 2001-10-12
? PRIOR APPLICATION NUMBER: US 6,023,972
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 5
? LENGTH: 181
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-975-901-5

```

```

Query Match
Best Local Similarity 56.5%; Score 35; DB 5; Length 181;
Matches 5: Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 4 SCSIASNYV 13
1 |1111111111111111
DB 19 SCSVANNWIE 28

```

```

RESULT 12
US-09-975-901-4
? SEQUENCE: Application US/09975901

```


THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: November 19, 2001, 08:13:25 ; Search time 43.5 seconds
(without alignments)
6.725 Million cell updates/sec

Title: US-09-610-118-64

Perfect score: 62

Sequence: 1 TRSSCSINSTVQ 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22502922 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database : Issued:Patents:AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	39	62.9	13	1 US-07-988-925-4	Sequence 4, Appl1
2	39	62.9	13	2 US-08-362-780-4	Sequence 16, Appl1
3	39	62.9	110	1 US-06-363-723-16	Sequence 16, Appl1
4	39	62.9	110	2 US-06-363-723-16	Sequence 16, Appl1
5	39	62.9	110	2 US-08-363-780-26	Sequence 26, Appl1
6	38	61.3	505	5 PCT-US95-05008-17	Sequence 17, Appl1
7	35	56.5	132	2 US-08-649-991-91	Sequence 91, Appl1
8	35	56.5	132	2 US-08-649-991-92	Sequence 92, Appl1
9	35	56.5	512	5 PCT-US95-05008-16	Sequence 16, Appl1
10	34	54.8	29	4 US-09-070-504-1	Sequence 1, Appl1
11	34	54.8	29	4 US-09-070-504-1	Sequence 1, Appl1
12	34	54.8	37	1 US-08-233-389C-9	Sequence 9, Appl1
13	34	54.8	37	2 US-08-801-863-9	Sequence 9, Appl1
14	34	54.8	37	2 US-08-486-596A-9	Sequence 9, Appl1
15	34	54.8	37	2 US-09-004-713-9	Sequence 2, Appl1
16	34	54.8	37	2 US-08-619-841-2	Sequence 2, Appl1
17	34	54.8	37	2 US-08-486-596A-2	Sequence 2, Appl1
18	34	54.8	37	2 US-08-486-596A-2	Sequence 2, Appl1
19	34	54.8	37	4 US-09-070-504-8	Sequence 8, Appl1
20	34	54.8	37	4 US-09-070-504-9	Sequence 9, Appl1
21	34	54.8	37	6 5424221-4	Patent No. 5424221
22	34	54.8	38	1 US-07-776-272-20	Sequence 20, Appl1
23	34	54.8	98	1 US-08-211-202-111	Sequence 111, Appl1
24	34	54.8	98	2 US-08-665-402-38	Sequence 38, Appl1
25	34	54.8	109	1 US-08-276-552-147	Sequence 147, Appl1
26	34	54.8	109	1 US-08-276-552-147	Sequence 147, Appl1
27	34	54.8	109	1 US-08-899-575-147	Sequence 147, Appl1

28	34	54.8	109	4 US-09-240-274-59	Sequence 59, Appl1
29	34	54.8	109	4 US-09-240-274-59	Sequence 59, Appl1
30	34	54.8	109	4 US-09-025-769B-51	Sequence 51, Appl1
31	34	54.8	109	5 PCT-US95-08743-147	Sequence 147, Appl1
32	34	54.8	110	4 US-09-240-274-60	Sequence 60, Appl1
33	34	54.8	111	4 US-08-983-607-21	Sequence 21, Appl1
34	34	54.8	111	4 US-08-983-607-21	Sequence 21, Appl1
35	34	54.8	113	1 US-08-211-202-113	Sequence 113, Appl1
36	34	54.8	113	1 US-08-211-202-113	Sequence 113, Appl1
37	34	53.2	37	4 US-09-070-504-10	Sequence 10, Appl1
38	34	53.2	37	4 US-09-070-504-10	Sequence 10, Appl1
39	33	53.2	142	2 US-08-480-774A-2	Sequence 2, Appl1
40	33	53.2	187	1 US-08-480-774A-2	Sequence 2, Appl1
41	33	53.2	332	4 US-09-321-581-23	Sequence 23, Appl1
42	33	53.2	431	2 US-08-665-647-5	Sequence 5, Appl1
43	33	53.2	588	1 US-08-391-615-9	Sequence 5, Appl1
44	33	53.2	691	1 US-08-178-477B-2	Sequence 2, Appl1
45	33	53.2	1196	1 US-08-861-706-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-988-925-4
Sequence 4, Application US/07988925
US-07-988-925-4
GENERAL INFORMATION:
APPLICANT: Bolt, Sarah L
APPLICANT: Clark, Michael R
APPLICANT: Gorman, Scott D
APPLICANT: Routledge, Edward G
APPLICANT: Waldmann, Herman
INVENTOR: Waldmann, Herman
NUMBER OF SEQUENCES: antibody preparation
ADDRESSER: Nixon and Vanderhye pc
STREET: 11th Floor, 1100 No. 585097th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,925
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/GB92/01933
APPLICATION NUMBER: NO PCT/GB92/01933
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQUENCE NO. 4:
SYNOPSIS CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-988-925-4

Query Match 62.9%: Score 39; DB 1; Length 13;
Best Local Similarity 66.7%: Pred. No. 0.26;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNY 12

DB 1 TLSSGSIENNY 12

RESULT 2

US-08-362-780-4

Patent No. 5968509

GENERAL INFORMATION:

APPLICANT: Gorman, Scott D

APPLICANT: Routledge, Edward G

APPLICANT: Waldmann, Herman

TITLE OF INVENTION: Antibody Preparation

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSER: Nixon and Vandervhe PC

STREET: 8th Floor, 1100 No. 5968509th Glebe Road

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,780

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/862,543

FILING DATE: 23-JUNE-1992

APPLICATION NUMBER: GB 9021679.7

FILING DATE: 05-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9021679.7

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mitchell, Leonard C

REGISTRATION NUMBER: 29009

TELEPHONE: 7038164000

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-362-780-4

APPLICANT: Bolt, Sarah L

APPLICANT: Clark, Michael R

APPLICANT: Gorman, Scott D

APPLICANT: Routledge, Edward G

APPLICANT: Waldmann, Herman

TITLE OF INVENTION: Antibody Preparation

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSER: Nixon and Vandervhe PC

STREET: 11th Floor, 1100 No. 5968509th Glebe Road

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/988,925

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206422.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB92/01933

FILING DATE: 21-OCT-1992

APPLICATION NUMBER: GB 9021679.7

FILING DATE: 05-OCT-1990

NAME: Mitchell, Leonard C

REGISTRATION NUMBER: 29009

TELEPHONE: 7038164000

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-988-925-16

Query Match 62.9%: Score 39; DB 1; Length 110;
Best Local Similarity 66.7%: Pred. No. 3.1;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRSSGSIASNY 12

DB 23 TLSSGSIENNY 34

RESULT 4

US-08-362-780-16

Patent No. 5968509

GENERAL INFORMATION:

APPLICANT: Gorman, Scott D

APPLICANT: Routledge, Edward G

APPLICANT: Waldmann, Herman

TITLE OF INVENTION: Antibody Preparation

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSER: Nixon and Vandervhe PC

STREET: 8th Floor, 1100 No. 5968509th Glebe Road

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05008-17

Query Match 61.3% Score 38; DB 5; Length 505;
Best Local Similarity 66.7% Pred. No. 27;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Y 1 TRSSGSIASNY 12
DB 101 TRKEGCIPTSNV 112

RESULT 7
US-08-649-991-91
Sequence 91; Application US/08649991
Patent No. 5919462
GENERAL INFORMATION:

APPLICANT: Narva, Remy
TITLE OF INVENTION: NOCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR
APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS & BOKKUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
TELEPHONE: 202-467-7176

TELEFAX: 202-467-7000
APPLICATION DATA:
FILING DATE: 17-MAY-1996

CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 9505914

FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: G. 30,988

REFERENCE/DOCKET NUMBER: ORES-5003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000

TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-991-91

Query Match 56.5% Score 35; DB 2; Length 132;
Best Local Similarity 54.5% Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Y 1 TRSSGSIASNY 11
DB 122 TRSSGVSQSNV 132

RESULT 8

US-08-649-991-92
Sequence 92; Application US/08649991
Patent No. 5919462
GENERAL INFORMATION:

APPLICANT: Narva, Remy
TITLE OF INVENTION: NOCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR
APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS & BOKKUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/649,991
FILING DATE: 17-MAY-1996
CLASSIFICATION: 435

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 9505914
FILING DATE: 18-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988

REFERENCE/DOCKET NUMBER: ORES-5003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176

TELEFAX: 202-467-7000
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-991-92

Query Match 56.5% Score 35; DB 2; Length 132;
Best Local Similarity 54.5% Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Y 1 TRSSGSIASNY 11
DB 122 TRSSGVSQSNV 132

RESULT 9
US-08-649-991-92
Sequence 92; Application US/08649991
Patent No. 5919462
GENERAL INFORMATION:

APPLICANT: Sugen, Inc.
TITLE OF INVENTION: NOCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR
APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS & BOKKUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/649,991
FILING DATE: 17-MAY-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 9505914
FILING DATE: 18-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: ORES-5003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7176

TELEFAX: 202-467-7000
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-991-92

```

? STREET: 1155 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: U.S.A.
? ZIP: 10036
? COMPUTER READABLE FORM:
?   COMPUTER: IBM PC compatible
?   OPERATING SYSTEM: PC-DOS/MS-DOS
?   SOFTWARE: Patent Release #1.0, Version #1.25
?   CURRENT APPLICATION NUMBER: PCT/US95/05008
?   FILING DATE: 24-APR-1995
? CLASSIFICATION:
?   PRIOR APPLICATION DATA:
?     APPLICATION NUMBER: US 08/232,545
?     FILING DATE: 22-APR-1994
? CLASSIFICATION:
?   ATTORNEY/AGENT INFORMATION:
?     NAME: Cortuzzi, Laura A.
?     REGISTRATION NUMBER: 30,742
?     TELECOMMUNICATION INFORMATION:
?       TELEPHONE: (212)869-9741
?       TELEFAX: (212)869-9741
?       TELEX: 66141 PENNIE
?     INFORMATION FOR SEQ ID NO: 16:
?       SEQUENCE CHARACTERISTICS:
?         LENGTH: 512 amino acids
?         TYPE: amino acid
?         STRANDEDNESS: unknown
?         TOPOLOGY: unknown
?     MOLECULE TYPE: protein
?     PCT-US95-05008-16

Query Match
Best Local Similarity: 56.58; Score 35; DB 5; Length 512;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 TRSSGSISNVY 12
DB 107 TKKEGFSINNV 118

RESULT 10
US-09-070-504-1
? Sequence 1, Application US/09070504
? Patent No. 6268474
? GENERAL INFORMATION:
?   APPLICANT: Smith, Derek D.
?   APPLICANT: Saha, Shankar
?   APPLICANT: Abel, Peter W.
?   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
?   NUMBER OF SEQUENCES: 23
?   CORRESPONDENCE ADDRESS:
?     ADDRESS: Mueller, Raasch & Gebhardt, P. A.
?     STREET: 119 No. 6268474th Fourth Street
?     CITY: Minneapolis
?     STATE: MN
?     COUNTRY: USA
?     ZIP: 55401
? COMPUTER READABLE FORM:
?   COMPUTER: IBM PC compatible
?   OPERATING SYSTEM: PC-DOS/MS-DOS
?   SOFTWARE: Patent Release #1.0, Version #1.30
?   CURRENT APPLICATION DATA:
?     APPLICATION NUMBER: US/09/070,504
?     FILING DATE: 30-APR-1998
? CLASSIFICATION:
?   ATTORNEY/AGENT INFORMATION:

```

```

? NAME: McCormack, Myra H
? REGISTRATION NUMBER: 36,602
? REFERENCE/DOCKET NUMBER: 180,00020101
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: 612/305-1220
?   TELEFAX: 612/305-1220
?   INFORMATION FOR SEQ ID NO: 1:
?     SEQUENCE CHARACTERISTICS:
?       LENGTH: 29 amino acids
?       TYPE: amino acid
?       STRANDEDNESS: single
?       TOPOLOGY: linear
?     MOLECULE TYPE: peptide
?     US-09-070-504-1

```

```

Query Match
Best Local Similarity: 54.88; Score 34; DB 4; Length 29;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 TRSSGSISNVY 12
DB 9 SRSCGVASNVY 20

RESULT 11
US-09-070-504-2
? Sequence 2, Application US/09070504
? Patent No. 6268474
? GENERAL INFORMATION:
?   APPLICANT: Smith, Derek D.
?   APPLICANT: Saha, Shankar
?   APPLICANT: Abel, Peter W.
?   TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
?   NUMBER OF SEQUENCES: 23
?   CORRESPONDENCE ADDRESS:
?     ADDRESS: Mueller, Raasch & Gebhardt, P. A.
?     STREET: 119 No. 6268474th Fourth Street
?     CITY: Minneapolis
?     STATE: MN
?     COUNTRY: USA
?     ZIP: 55401
? COMPUTER READABLE FORM:
?   COMPUTER: IBM PC compatible
?   OPERATING SYSTEM: PC-DOS/MS-DOS
?   SOFTWARE: Patent Release #1.0, Version #1.30
?   CURRENT APPLICATION DATA:
?     APPLICATION NUMBER: 09/070,504
?     FILING DATE: 30-APR-1998
? CLASSIFICATION:
?   ATTORNEY/AGENT INFORMATION:

```

```

? NAME: McCormack, Myra H
? REGISTRATION NUMBER: 36,602
? REFERENCE/DOCKET NUMBER: 180,00020101
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: 612/305-1220
?   TELEFAX: 612/305-1220
?   INFORMATION FOR SEQ ID NO: 2:
?     SEQUENCE CHARACTERISTICS:
?       LENGTH: 30 amino acids
?       TYPE: amino acid
?       STRANDEDNESS: single
?       TOPOLOGY: linear
?     MOLECULE TYPE: peptide
?     US-09-070-504-2

```

```

Query Match
Best Local Similarity: 54.88; Score 34; DB 4; Length 30;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

OY 1 TRSSGSIASNVY 12
 :|||:|:|:|
 Db 9 SRSOGVMSNV 20

RESULT 12
 US-08-233-389C-9
 : Sequence 9, Application US/08233389C
 : Patent No. 5619855
 : GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo
 APPLICANT: KANGAWA, Kenji
 APPLICANT: MATSUO, Hisayuki
 APPLICANT: MATSUO, Hisayuki
 TITLE OF INVENTION: ADRENOMEDULLIN
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS: 10
 ADDRESSEE: C/O FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York

STATE: NY
 ZIP: 10020
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/233,389C
 FILING DATE: 26-Apr-1994
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: HALEY JR., James F.
 REGISTRATION NUMBER: 27,794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids
 TOPOLOGY: Linear
 MOLECULE TYPE: protein

US-08-233-389C-9

Query Match 54.8% Score 34: Db 1: Length 37:
 Best Local Similarly 50.0%: Prod No. 7.4:
 Matches 0: Conservative 3: Mismatches 3: Indels 0: Gaps 0:

OY 1 TRSSGSIASNVY 12
 :|||:|:|:|
 Db 17 SRSOGVMSNV 28

RESULT 13
 US-08-801-863-9
 : Sequence 9, Application US/0801863
 : Patent No. 5830703
 : GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo
 APPLICANT: KANGAWA, Kenji
 APPLICANT: MATSUO, Hisayuki
 APPLICANT: MATSUO, Hisayuki
 TITLE OF INVENTION: ADRENOMEDULLIN
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS: 10
 ADDRESSEE: C/O FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: NY

COUNTRY: USA
 ZIP: 10020
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,863
 FILING DATE: CONCURRENTLY HERewith
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: HALEY JR., James F.
 REGISTRATION NUMBER: 27,794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids
 TOPOLOGY: Linear
 MOLECULE TYPE: protein

US-08-801-863-9

Query Match 54.8% Score 34: Db 2: Length 37:
 Best Local Similarly 50.0%: Prod No. 7.4:
 Matches 6: Conservative 3: Mismatches 3: Indels 0: Gaps 0:

OY 1 TRSSGSIASNVY 12
 :|||:|:|:|
 Db 17 SRSOGVMSNV 28

RESULT 14
 US-08-486-596A-9
 : Sequence 9, Application US/08486596A
 : Patent No. 5837823
 : GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo
 APPLICANT: KANGAWA, Kenji
 APPLICANT: MATSUO, Hisayuki
 APPLICANT: MATSUO, Hisayuki
 TITLE OF INVENTION: ADRENOMEDULLIN
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS: 10
 ADDRESSEE: C/O FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: NY

COUNTRY: USA
 ZIP: 10020
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,596A
 FILING DATE: JUNE 7, 1995
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: HALEY JR., James F.
 REGISTRATION NUMBER: 27,794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids

; rfr: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-486-596A-9

Query Match 54.8%; Score 34; DB 2; Length 37;
 Best Local Similarity 50.0%; Pred. No. 7.4;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNRY 12
 :|||:||||
 Db 17 SRSGCWYKSNRY 28

RESULT 15
 US-09-004-713-9
 ; Sequence 9; Application US/09004713
 ; Patent No. 5910416
 ; GENERAL INFORMATION:
 ; APPLICANT: KITAHARA, Kazuo
 ; APPLICANT: KANGAWA, Kenji
 ; APPLICANT: MATSUO, Hisayuki
 ; APPLICANT: SHIMIZU, Kenji
 ; TITLE OF INVENTION: DENDROCHEMULIN
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: C/O FISH & NEAVE
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: SEQEDIT; Release #1.0; Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/004,713
 ; FILING DATE: JANUARY 7, 1998
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HALEY JR., James F.
 ; FIRM: HALEY JR., JAMES F. & ASSOCIATES
 ; ADDRESS: 1000 UNIVERSITY BLVD., SUITE 500
 ; TELEPHONE: (212) 596-9000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 596-9000
 ; TELEFAX: (212) 596-9090
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 37 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-004-713-9

Query Match 54.8%; Score 34; DB 2; Length 37;
 Best Local Similarity 50.0%; Pred. No. 7.4;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TRSSGSIASNRY 12
 :|||:||||
 Db 17 SRSGCWYKSNRY 28

Search completed: November 19, 2001, 08:13:25
 Job time: 138 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: November 19, 2001, 08:12:35 ; Search time 77.92 seconds
(Without alignments)
5.446 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EMDORPS 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Minimum Match 11008

Listing first 45 summaries

Database :

A_Geneseq_0601:*

1: /SID88/gcgcata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgcata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgcata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgcata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgcata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgcata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgcata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgcata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgcata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgcata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgcata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgcata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgcata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgcata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgcata/geneseq/geneseq/AA1995.DAT.*
16: /SID88/gcgcata/geneseq/geneseq/AA1996.DAT.*
17: /SID88/gcgcata/geneseq/geneseq/AA1997.DAT.*
18: /SID88/gcgcata/geneseq/geneseq/AA1998.DAT.*
19: /SID88/gcgcata/geneseq/geneseq/AA1999.DAT.*
20: /SID88/gcgcata/geneseq/geneseq/AA2000.DAT.*
21: /SID88/gcgcata/geneseq/geneseq/AA2001.DAT.*
22: /SID88/gcgcata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	38	100.0	7	AA661297	Anti-TANCO 268 scf
2	34	89.5	106	AA54054	Sequence of the VI
3	34	89.5	106	AA54054	Monoclonal antibody
4	34	89.5	106	AA54054	Monoclonal antibody
5	34	89.5	106	AA54054	Monoclonal antibody
6	34	89.5	109	AA16588	Anti-NSV F glycopr
7	34	89.5	109	AA16588	Human monoclonal a
8	34	89.5	114	AA53654	Human colon cancer
9	33	86.6	112	AA50488	56 human sfp anti
10	33	86.6	112	AA50488	56 human sfp anti
11	32	84.2	108	AA601523	Monoclonal antibody

12	32	84.2	108	AA62498	Monoclonal antibody
13	31	81.6	109	AA68998	Anti-TANCO 268 scf
14	31	81.6	109	AA68998	Anti-TANCO 268 scf
15	31	81.6	108	AA68990	Variable region of
16	30	78.9	109	AA627547	Human A1 light cha
17	30	78.9	151	AA62871	Arbidoposits thall
18	30	78.9	155	AA62451	Adenovirus E1A-F p
19	30	78.9	158	AA63874	S. pneumoniae derl
20	30	78.9	161	AA63870	Arbidoposits thall
21	30	78.9	462	AA600167	Human poliovirus
22	30	78.9	462	AA600167	Human poliovirus
23	30	78.9	462	AA600167	Human poliovirus
24	30	78.9	555	AA649010	Polymavirus PEA3
25	30	78.9	555	AA649010	Polymavirus PEA3
26	30	78.9	555	AA649010	Polymavirus PEA3
27	30	78.9	620	AA649010	Mouse PER-3 protei
28	30	78.9	620	AA649010	Mouse PER-3 protei
29	30	78.9	620	AA649010	Mouse PER-3 protei
30	30	78.9	620	AA649010	Mouse PER-3 protei
31	30	78.9	858	AA671997	Rat autotaxin vari
32	30	78.9	858	AA671997	Rat autotaxin vari
33	30	78.9	858	AA671997	Rat autotaxin vari
34	30	78.9	858	AA671997	Rat autotaxin vari
35	29	76.3	98	AA64013	Rat brain autotaxi
36	29	76.3	119	AA64013	Anti-TIL12 antibody
37	29	76.3	119	AA64013	Anti-TIL12 antibody
38	29	76.3	112	AA613528	Anti-melanoma ligh
39	29	76.3	129	AA613528	Human monoclonal a
40	29	76.3	132	AA613528	Human ARF-p19, a n
41	29	76.3	132	AA613528	Human ARF-p19, a n
42	29	76.3	202	AA670119	Human p15 encoded
43	29	76.3	202	AA670119	Human p15 encoded
44	29	76.3	202	AA670119	Human p15 encoded
45	29	76.3	260	AA647236	Arbidoposits thall

ALIGNMENTS

RESULT 1	AA661297	standard: Peptide: 7 AA.
XX	AA661297	
AC	AA661297	
XX	AA661297	
DT	04-APR-2001	(first entry)
XX	AA661297	
DE	Anti-TANCO 268 scf CDR, SEQ ID NO: 65.	
KW	Human: antibody; scfv; CDR; complementarily determining region;	
KW	TANCO 268; carianti; cerebroprotective; cytostatic; anticoagulant;	
KW	thrombolytic; antiarteriosclerotic; hemostatic; glycoprotein VI; Gvvi;	
KW	platelet membrane glycoprotein receptor; bleeding disorder;	
KW	ischemia; injury; thrombotic disorder; haemorrhagic disorder; stroke;	
KW	ischemia; cardiovascular disease; immunological disease; liver disorder;	
XX	cancer.	
OS	Human sapiens.	
XX	WO200100810-A1.	
PN	04-JAN-2001.	
XX	30-JUN-2000; 2000MO-US18152.	
PR	30-JUN-1999; 99US-0345468.	
PR	06-DEC-1999; 99US-0454824.	
PR	14-FEB-2000; 2000US-050387.	
XX	(MILL-) MILLERIN PHARM INC.	
XX	Bufield SJ, Villeda J, Jandrot-Perrus M, Valinchenker W, Gill DS;	
PI	Qlan MO, Kingsbury G;	

[illegible]

XX	This peptide sequence comprises complementarity determining region CC
CC	(CDR2) of the light chain VL6 region of a novel neutralising
OC	human monoclonal antibody to the respiratory syncytial virus (RSV).
CC	The body, designated RSVF2-5 (NC 6909), selectively binds to
CC	an RSV F protein epitope (AA16587-94) encoding RSVF2-5 pd and lignt
CC	chain (see AA16586-57). We could also obtain a highly purified
CC	donor. A claimed pharmaceutical preparation comprises a carrier
CC	from the RNA of peripheral blood lymphocytes or an HIV+ patient.
CC	and an antibody that includes the VHS CDR2 (AA116584) and/or CDR1 (AA116582)
CC	which may also include the VH3 CDR2 (AA116584) and/or CDR1 (AA116582)
CC	of the entire rd region (AA116580), CDR2, CDR1 (AA116590) or entire
CC	light chain (AA16588).
CC	A vector that includes a nucleotide encoding at least one of
CC	the antibody . The preparations can be used for the treatment of
CC	propylaxis of active RSV disease or infection (claimed), and may
CC	also be used for RSV detection. The antibody binds and neutralises
XX	antigenic subgroups A and B of RSV with high efficiency.
XX	
SQ	Sequence 7 AA:
	Query Match 89.5%; Score 34; DB 18; Length 7;
	Best Local Similarity 100.0%; Pred. No. 3, 4e-05;
	Matches Conservative 0; Mismatches 0; Gaps 0;
OY	1 EDDNP 6
Dd	1 ednqp 6
RESULT 3	
AAKS4054	Standard: Protein; 106 AA.
XI	
ID	AAKS4054:
XC	
XX	08-NOV-1994 (first entry)
DE	
DE	Sequence of the VL region of monoclonal antibody MD3-4 against
XS	Hepatitis B virus surface antigen.
KX	Hepatitis B virus; surface antigen; monoclonal antibody; therapy;
KM	HBsAg; diagnosis; HBV.
OS	xx
XS	synthetic.
FH	Key
FT	Region
FT	Location/Qualifiers
FT	1..95
FT	/label= V III
FT	24..33
FT	/label= CDR 1
FT	50..56
FT	/label= CDR 2
FT	88..96
FT	/label= CDR 3
FT	95..106
FT	/label= J 3
PM	
PN	MO9A11495-A.
PD	26-MAY-1994.
PD	
PF	06-NOV-1992; 92NO-USO9749.
PA	06-NOV-1992; 92NO-USO9749.
PA	(SANO) SANOZ LTD.
PI	Ostberg LG;
WFI	1994-1834497/22.

DR N-PSDB: AM064057.
 XX Monoclonal antibodies active against Hepatitis B surface antigen
 XX - for diagnosis and treatment of Hepatitis B virus
 PS Example: Page 43; 53pp; English.
 XX Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZM1-
 CC 2, ZM1-1 and PE1-1 hybridoma cell lines were derived from
 CC lymphocytes of individuals immunised with Hepavax (Merck & Co)
 CC The cell lines producing ZM1-1, ZM1-2 and ZM1-3 were deposited as
 CC ATCC HB9234, 9191 and 9192 respectively. The cell lines all behave
 CC as typical (mouse x human) x human hybridomas and produce their
 CC respective Abs in concs. ranging up to 25 mg/l in standard (LH)
 CC suspension culture. The heavy variable (VH) and light variable (LH)
 CC chains of Abs PE1-1, ZM1-1, ZM1-2 and MD3-4 were isolated and
 CC sequenced. Total RNA was extracted from 10⁷ hybridoma cells
 CC and reverse transcribed. The cDNA was then amplified using
 CC transcriptase and oligo-dT as primer. PCR were performed and
 CC amplified DNA was size selected. ss DNA for sequencing was isolated
 CC from each positive clone after superinfection with M13K07.
 CC Sequencing was by the dideoxy chain termination method (Sanger
 CC et al.).
 XX Sequence 106 AA:
 SQ
 Query Match 89.5%; Score 34; DB 15; Length 106;
 Best Local Similarity 85.7%; Pred. No. 8;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 EDNORPS 7
 DB 49 ednkrps 55
 RESULT 4
 ID AAM01529 standard; Protein: 106 AA.
 XX AAM01529:
 DE 04-MAR-1997 (first entry)
 XX Monoclonal antibody MD3-4 light chain variable region.
 XX
 KM Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
 KM xenogeneic hybridoma; SPZ 4; PE1-1; ZM1-1; ZM1-2; MD3-4; L03-3;
 KM 1991 class; heavy chain; light chain; variable region.
 XX
 OS Homo sapiens.
 FH Key location/Qualifiers
 FH Region /label=V_kappa-III_region
 FT 24..33- CDR1
 FT 34..49
 FT Region /label=framework_region
 FT 50..56
 FT Region /label=CDR2
 FT 57..87
 FT Region /label=framework_region
 FT 88..93
 FT Region /label=CDR3
 FT 95..106
 FT Region /label=J_kappa-3_region
 XX
 XX US5565354-A.
 XX
 XX 15-OCT-1996.

PE 05-SEP-1986; 8605-0904517.
 XX 21-APR-1992; 9205-0871426
 XX 05-SEP-1986; 8605-0904517.
 PR 31-OCT-1986; 8605-0925196.
 PR 11-MAY-1988; 8805-0192754.
 PR 15-JUN-1990; 9005-0538796.
 PR 27-MAR-1991; 9105-0676036.
 PR 14-JUN-1994; 9405-0259372.
 XX (SANO) SANOZ LTD.
 XX
 PI Ostberg IG;
 DR WPI: 1996-476304/47.
 N-PSDB: AAT6135.
 XX human monoclonal antibodies specific for hepatitis B surface antigen
 PS - are used to treat or prevent infection or in diagnostic assays
 XX Example 9; Column 43-46; 26pp; English.
 XX Monoclonal antibodies effective for the diagnosis and treatment of
 CC diseases caused by infection with hepatitis B have been prepared from a
 CC cell line obtained from a patient immunised with hepatitis B vaccine
 CC with the aid of a panel of monoclonal antibodies specific for hepatitis B
 CC Specific antibodies are PE1-1, ZM1-1, ZM1-2, MD3-4 and L03-3, each of
 CC these being of the IgG1 class. The present sequence is the light
 CC variable chain of MD3-4.
 XX Sequence 106 AA:
 SQ
 Query Match 89.5%; Score 34; DB 17; Length 106;
 Best Local Similarity 85.7%; Pred. No. 8;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 EDNORPS 7
 DB 49 ednkrps 55
 RESULT 5
 ID AAM24991 standard; Protein: 106 AA.
 XX AAM24991:
 AC 08-DEC-1997 (first entry)
 DE Monoclonal antibody MD3-4 VL region.
 XX
 KM Heavy chain; light chain; variable region; human; monoclonal antibody;
 KM immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; xenogeneic;
 KM peripheral blood lymphocyte; surface antigen; cell culture; ion exchange;
 KM chromatography; size separation; primer; PCR; polymerase chain reaction;
 KM amplification; hybridoma; infection; immunosuppression; hepatitis;
 KM liver transplant.
 XX
 OS Homo sapiens.
 FH Key location/Qualifiers
 FH Region /note="VIII region"
 FT 1..94
 FT Domain /note="complementarity determining region 1"
 FT 50..56
 FT Domain /note="complementarity determining region 2"
 FT 88..96
 FT Domain /note="complementarity determining region 3"
 FT 95..106
 FT Region /note="J13 region"
 XX

FN US5648077-A.
 XX 15-JUL-1997.
 XX
 PE 05-SEP-1986; 86US-0904517.
 XX
 PR 21-APR-1992; 92US-0871426.
 XX 05-SEP-1986; 86US-0904517.
 PR 31-OCT-1986; 86US-0925196.
 XX 12-MAR-1989; 88US-0192724.
 PR 27-MAR-1993; 91US-0676036.
 PR 14-JUN-1994; 94US-0259372.
 PR 06-JUN-1995; 95US-0468671.
 XX (SANO) SANDOZ LTD.
 XX
 XX Ostberg LG:
 XX WPI: 1997-272021/34.
 DR N-PSDB: AAT65845.
 XX
 XX Treatment of hepatitis B - with human monoclonal antibody
 PT
 PR
 XX
 XX Example 8: Column 23-24; 25pp; English.
 XX
 CC This is the amino acid sequence of the light chain variable (V1) region
 CC from the human monoclonal antibody (Mab) M13. The Mab was prepared
 CC by immunising humans with a hepatitis B virus (HBV) vaccine, isolated
 CC from peripheral blood lymphocytes (PBL) and fusing them with a mouse/human
 CC xenogeneic cell line SP2-4. 5 cell lines were then tested for production
 CC of anti-hepatitis B virus surface antigen antibody by ELISA. The Mabs
 CC are the anti-hepatitis B virus surface antigen antibody protein A
 CC chromatography, size separation and cell culture supernatant and for exchange
 CC chromatography on Q-sepharose. The heavy and light chains of the
 CC were isolated and their amino acid sequences determined. Primers were
 CC generated and used to amplify cDNA synthesised from RNA purified from
 CC each hybridoma cell line. The sequences of the heavy and light chains
 CC (nucleic acid and amino acid) from Mabs PE1-1, ZM1-1, ZM1-2 and MD3-4
 CC are shown in SEQ-IDS 43 and AAM2984-91. The Mabs can be used to treat
 CC HBV infections in humans and in animal models of patients with chronic
 CC active hepatitis, especially liver transplant patients.
 XX
 XX Sequence 106 AA:
 SQ
 Query Match 89.5%; Score 34; DB 18; Length 106;
 Best Local Similarity 85.7%; Pred. No. 8.3;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNQRS 7
 DB 49 cdoktps 55
 XX
 XX RESULT 6
 XX AAM15588
 XX ID AAM15588 standard; Protein: 109 AA.
 XX AAM15588;
 XX 30-NOV-1997 (first entry)
 XX
 DE Anti-RSV F glycoprotein antibody RSVF2-5 Light chain V16.
 XX
 XX Respiratory syncytial virus: RSV; monoclonal antibody: CDR;
 KW complementarity determining region: pneumonia; bronchiolitis;
 KW diagnosis: therapy; vaccine; RSVF2-5.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT Peptide 1..19
 FT /label= PRL
 FT /note= "framework region 1"
 FT Region 20..32
 FT /label= CDR1
 FT /note= "complementarity determining region 1
 FT Region 33..47
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 48..54
 FT /label= CDR2
 FT /note= "complementarity determining region 2
 FT Region 55..88
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 89..98
 FT /label= CDR3
 FT /note= "complementarity determining region 3
 FT Region 99..109
 FT /label= FR4
 FT /note= "framework region 4"
 XX
 XX MO971084-6-A1.
 XX
 XX 27-MAR-1997.
 XX
 XX 18-SEP-1996; 96NO-US14937.
 XX
 XX 18-SEP-1995; 95US-0003931.
 XX
 XX (INTR-) INTRACEL CORP.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Chanock RM, Crome JF, Gilmour FS, Murphy BR, Pilkington GR;
 XX WPI: 1997-202621/18.
 XX N-PSDB: AAT6557.
 XX
 DR Composition comprising respiratory syncytial virus antibody - useful
 DR for treatment or prophylaxis of active disease or infection
 XX
 PT Claim 10: Page 52-53; 71pp; English.
 PT
 XX
 XX This polypeptide sequence comprises the light chain V16 region
 CC of a novel neutralising human monoclonal antibody to respiratory
 CC syncytial virus (RSV). The antibody, designated RSVF2-5 (ATCC
 CC 63909), selectively binds to an RSV F glycoprotein epitope. cDNA
 CC encoding the RSVF2-5 Fd VH3 and light chain V16 (see AAT6556-57)
 CC was used to produce a recombinant antibody. The antibody was
 CC the peripheral blood lymphocytes of a patient prepared from RNA extracted from
 CC claimed pharmaceutical preparation comprises a carrier and an
 CC antibody that includes the RSVF2-5 VH3 CDR3 (AAM15586) and which may
 CC also include the VH3 CDR2 (AAM15584) and/or CDR1 or the entire Fd
 CC Fd region (AAM15580), or is an Fdb fragment and further includes the
 CC RSVF2-5 L6 CDR3 (AAM15594), CDR2 (AAM15592), CDR1 (AAM15590) or entire
 CC light chain (AAM15588) and/or a vector that includes at least one of the
 CC the antibody. The preparations can be used for the treatment or
 CC prophylaxis of active RSV disease or infection (claimed), and may
 CC also be used for RSV detection. The antibody binds and neutralises
 CC antigenic subgroups A and B of RSV with high efficiency.
 XX
 XX Sequence 109 AA:
 SQ
 Query Match 89.5%; Score 34; DB 18; Length 109;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNQRP 6

DB 48 edngrp 53

RESULT 7
AA14785
ID AA14785 standard; Protein: 109 AA.
XX
XX AA14785;
XX
XX 20-JUN-1997 (first entry)
XX
XX Human monoclonal antibody RSVF2-5 light chain VL6.
DE
XX Respiratory syncytial virus; RSV; monoclonal antibody; MB:
KM diagnosis; prophylaxis; immunotherapy; Fab; Fd.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT Region 1..19
FT /label= FRI
FT Region 20..32
FT /label= CDR1
FT /note= "Claim 9"
FT 33..47
FT /label= FRI
FT 48..54
FT /label= CDR2
FT /note= "Claim 8"
FT Region 55..88
FT /label= FRI
FT Region 89..98
FT /label= CDR3
FT /note= "Claim 7"
FT 99..109
FT /label= FRI
XX
XX Region
XX
XX
XX NO971177-A1.
XX
XX 27-MAR-1997.
XX
XX 18-SEP-1996; 96MO-US14944.
XX
XX 18-SEP-1995; 95US-0003931.
XX
XX (INTR-) INTRACEL CORP.
XX
XX Gilmour PS; Plikington GR;
XX WPI: 1997-202886/18.
XX N-PSDB: AAT63418.
XX
XX Monoclonal antibody specific for respiratory syncytial virus - used
PT for diagnosis and immuno-prophylaxis or immuno-therapy of RSV
PT disease
PT
PS Claim 10; Page 49-50; 6pp; English.
XX
XX The light chain variable region (AA14785) and heavy chain variable
CC region (AA14784) are provided of a novel, fully human monoclonal
CC antibody (MAb), designated RSVF2-5, which selectively binds to
CC the F glycoprotein of respiratory syncytial virus (RSV) and which
CC is capable of neutralizing RSV. The MAb is derived from a hybridoma
CC library was prepared from amplified heavy and light chain variable
CC region clones derived from the peripheral blood lymphocytes of an
CC HIV-1 infected donor. The phage library was panned with RSV
CC proteins and isolated clones were sequenced. Isolated nucleic
CC acids (AAT63417-18) can be used to produce novel polypeptides, esp.
CC Fd or Fab fragments useful in the diagnosis of RSV disease, in
CC methods for detecting the presence of RSV in a sample, and in the
CC immunoprophylaxis and immunotherapy of RSV disease.
XX

SO Sequence 109 AA:
Query Match 89.5%; Score 34; ps 18; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNCRP 6
DB 48 edngrp 53

RESULT 8
AAB53654
ID AAB53654 standard; Protein: 114 AA.
XX
XX AAB53654;
XX
XX 09-MAR-2001 (first entry)
XX
XX Human colon cancer antigen protein sequence SEQ ID NO:1194.
DE
XX
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KM identification; cystic; cardiovascular; neuroprotective; vulnery;
KM immunomodulatory; muscular; gynecological; gas therapy; sound;
KM neural disorder; immune system disorder; muscular disorder;
KM reproductive disorder; gastrointestinal disorder; renal disorder;
KM infectious disease; cardiovascular disorder.
XX
XX Homo sapiens.
OS
XX
XX NO20005351-A1.
XX
XX 21-SEP-2000.
PD
XX 08-MAR-2000; 2000MO-US05883.
PE
XX 12-MAR-1999; 99US-0124270.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX N-PSDB: AAC98411.
XX WPI: 2000-587534/55.
XX
XX Colon cancer associated gene sequences, referred to as colon cancer
PT genes, are used for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer."
XX
XX
XX Claim 11; Page 1776; 2104pp; English.
XX
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53654. Colon cancer
CC is a leading cause of cancer death. Colon cancer is a disease of the
CC human protective immunomodulatory, gastroecological, gastrointestinal,
CC and vulnery, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC immunoscreening and for the development of vaccines. The polynucleo-
CC tides may be used to prevent diseases such as neural disorders, imune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, wounds, renal disorders, infectious
CC diseases, and cardiovascular disorders. AAC9794 to AAC98772 and
CC AAB54007 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 114 AA;
XX


```

Best Local Similarity 71.4%  Pred. No. 21:
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 EDNORPS 7
Db 49 ddnerps 55

RESULT 11
ID AAM01523 standard; Protein: 108 AA.
AC AAM01523;
XX
XX 04-MAR-1997 (first entry)
XX
XX Monoclonal antibody PEL-1 light chain variable region.
XX
XX Monoclonal antibody; diagnosis: treatment: infection: hepatitis B;
XX xenogeneic hybridoma; SP#2 4; PEL-1; ZM1-1; ZM1-2; MD3-4; L03-3;
XX IgG1 class; heavy chain; light chain; variable region.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..96
XX /label= VY_region
XX Region 24..30
XX /label= CDR1
XX Region 31..49
XX /label= Framework_region
XX Region 50..54
XX /label= CDR2
XX Region 55..89
XX /label= Framework_region
XX Region 90..98
XX /label= CDR3
XX Region 97..106
XX /label= J1_region
XX
XX US556334-A.
XX
XX 15-OCT-1996.
XX
XX 05-SEP-1986; 86US-0904517.
XX
XX 21-APR-1992; 92US-0871426.
XX 05-SEP-1986; 86US-0904517.
XX 31-OCT-1986; 86US-0925196.
XX 11-MAY-1988; 88US-0192754.
XX 15-JUN-1990; 90US-0538796.
XX 27-MAR-1991; 91US-0676036.
XX 14-JUN-1991; 91US-0676036.
XX 14-JUN-1995; 95US-0259372.
XX
XX (SANO ) SANDOZ LTD.
XX
XX Ostberg LG;
XX WPI: 1996-476304/47.
XX N-PSDB: AAT46129.
XX
XX Human monoclonal antibodies specific for hepatitis B surface antigen
XX - are used to treat or prevent infection or in diagnostic assays
XX
XX Claim 4; Column 37-38; 26pp; English.
XX
XX Monoclonal antibodies effective for the diagnosis and treatment of
XX diseases caused by hepatitis B. The antibodies B have been prepared from a
XX cell line obtained by fusing a xenogeneic hybridoma (SP#2 4
XX with blood cells of a patient immunised with hepatitis B
XX Specific antibodies are PEL-1, ZM1-1, ZM1-2, MD3-4 and L03-3. Each of
XX these being of the IgG1 class. The present sequence is the light
XX variable chain of PEL-1.

```

```

XX
XX Sequence 108 AA:
XX
XX Query Match 84.2% Score 32; DB 17; Length 108;
XX Best Local Similarity 71.4%  Pred. No. 21:
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 EDNORPS 7
Db 49 ddnerps 55

RESULT 12
ID AAM24988 standard; Protein: 108 AA.
AC AAM24988;
XX
XX 08-DEC-1997 (first entry)
XX
XX Monoclonal antibody PEL-1 VL region.
XX
XX Heavy chain; light chain; variable region; human; monoclonal antibody;
XX immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; xenogeneic;
XX peripheral blood lymphocyte; surface antigen; cell culture; ion exchange;
XX chromatography; size separation; primer; PCR; polymerase chain reaction;
XX liver transplant.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..96
XX /label= "V1V region"
XX Region 24..33
XX /note= "complementarity determining region 1"
XX Domain 50..56
XX /note= "complementarity determining region 2"
XX Domain 90..98
XX /note= "complementarity determining region 3"
XX Region 97..106
XX /note= "J13 region"
XX
XX US5648077-A.
XX
XX 15-JUL-1997.
XX
XX 05-SEP-1986; 86US-0904517.
XX
XX 21-APR-1992; 92US-0871426.
XX 05-SEP-1986; 86US-0904517.
XX 31-OCT-1986; 86US-0925196.
XX 11-MAY-1988; 88US-0192754.
XX 15-JUN-1990; 90US-0538796.
XX 27-MAR-1991; 91US-0676036.
XX 14-JUN-1991; 91US-0676036.
XX 14-JUN-1995; 95US-0468671.
XX
XX (SANO ) SANDOZ LTD.
XX
XX Ostberg LG;
XX WPI: 1997-372021/34.
XX N-PSDB: AAT5842.
XX
XX "Treatment of hepatitis B - with human monoclonal antibody
XX Example 8; Column 19-22; 25pp; English.
XX
XX This is the amino acid sequence of the light chain variable (VL) region
XX of the human monoclonal antibody (hAb) PEL-1. The sequence was generated
XX by immunising humans with a hepatitis B virus (HBV) vaccine, isolating

```

peripheral blood lymphocytes (PBL) and fusing them with a mouse/human
 CC X-CELL LINE SP2-0.5 cell lines were isolated. PEI-1, ZMI-1,
 CC ZMI-2, MD3-4 and LO3-3. The cell lines were then tested for production
 CC of an anti-hepatitis B virus surface antigen antibody by ELISA. The Mabs
 CC are then purified from large scale cell culture by protein A
 CC chromatography, size separation on Sephacryl S300 gel, and ion exchange
 CC chromatography on Q-Sepharose. The heavy and light chains of the Mabs
 CC were isolated and the heavy chain of the Mabs was used to amplify cDNA
 CC and the light chain of the Mabs was used to amplify cDNA synthesized from RNA
 CC extracted from each hybridoma cell line. The sequences of the heavy and light chains
 CC (nucleic acid and amino acid) from Mabs PEI-1, ZMI-1, ZMI-2 and MD3-4
 CC are shown in AAR85038-45 and AAM24994-91. The Mabs can be used to treat
 CC HBV infections in immunosuppressed patients or patients with chronic
 CC active hepatitis, especially liver transplant patients.

Sequence 108 AA:

Query Match 84.2%; Score 32; DB 18; Length 108;

Best Local Similarity 71.4%; Pred. No. 21;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENDORPS 7

DB 49 dndrps 55

RESULT 13

AAR8719

MD AAR8719 standard; protein; 108 AA.

AAR8719:

26-SEP-1996 (first entry)

Human antibody lambda chain variable region consensus sequence.

Antibody; stability; instability; antigenicity; amino acid frequency;

antibody; sequence approximation; subcloning; immunoglobulin;

light chain; variable region; V-region; diagnosis; immunoassay;

cancer treatment; autoimmune disease; immunotoxin; improved yield.

Homo sapiens.

DE4425115-A1.

18-JAN-1996.

15-JUL-1994; 94DE-4425115.

15-JUL-1994; 94DE-4425115.

(BOER) BOEHRINGER MANNHEIM GMBH.

Steinbacher S, Steipe B;

WPI; 1996-063934/08.

Punctal antibodies modified to increase or decrease stability -
 by reference to consensus sequences

Claim 2: Page 31; 43pp; German.

Consensus sequences were established for antibody variable regions
 from human and mouse heavy and light (kappa and lambda) chains in
 CC each position were compiled. In a new method, mutations are
 CC introduced into an antibody variable domain by reference to the
 CC frequency table. When an amino acid is replaced by one which occurs
 CC at a higher frequency at that position, the resulting amino chain
 CC is more stable than the wild-type; when an amino acid is replaced by
 CC one which occurs less frequently (or not at all), the resulting

antibody is less stable than the wild-type. Stabilised antibodies
 CC are useful as diagnostic reagents, as catalysts and in treatment of
 CC cancer, autoimmune diseases and infections. Destabilised antibodies
 CC have improved (faster) pharmacokinetic properties.
 CC The present sequence is the human lambda light chain variable region
 CC consensus sequence.

Sequence 108 AA:

Query Match 81.6%; Score 31; DB 17; Length 108;

Best Local Similarity 71.4%; Pred. No. 34;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ENDORPS 7

DB 49 dndrps 55

RESULT 14

AAR6898

MD AAR6898 standard; Protein; 108 AA.

AAR6898:

16-MAY-2000 (first entry)

The variable region of the light chain of HBAB503.

Variable light chain; human anti-HCV antibody; chronic hepatitis C;

conformation-dependent epitope; HCV glycoprotein E2; HCV infection;

liver transplantation; Tupaia-hepatocytes; HCV-infectious human sera.

Homo sapiens.

NC020005266-A1.

03-FEB-2000.

20-JUL-1999; 99NO-EP05173.

21-JUL-1998; 98EP-0113595.

(CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

(INRM) INSEMN INST NAT SANTE & RECH MEDICALE.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

WPI; 2000-182654/16.

CC In liver transplantation. The antibody is also useful for the prevention
 CC of infection of Tupaia-hepatocyte with HCV-infectious human sera.
 X
 X
 SQ Sequence 108 AA:

Query Match 81.6% Score 31: DB 21: Length 108:
 Best Local Similarity 71.4% Pred. No. 34:
 Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:
 OY 1 EDNORPS 7
 :||:||||
 Db 49 Kdnrps 55

RESUME 15

AA668900 standard; Protein; 108 AA.
 ID AA668900
 X
 X
 AC AA668900:

DT 16-MAY-2000 (first entry)

DE Variable region of the light chain of an anti-HCV antibody.

CC Variable light chain: human anti-HCV antibody; chronic hepatitis C;
 CC conformation-dependent epitope; HCV glycoprotein E2; HCV infection;
 KW liver transplantation; Tupaia-hepatocyte; HCV-infectious human sera.
 X
 X

OS Homo sapiens.

XX NO200005266-A1.

PD 03-FEB-2000.

PF 20-JUL-1999: 99MO-EP05173.

XX 21-JUL-1998: 98EP-0113595.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Reiter C, Habersetzer F, Fournillier A, Trepo C, Desgranges C;

XX WP1: 2000-182654/16.

DR W-ESDB: AA660761.

PT Novel antibodies, antigens, for diagnosing and treating hepatitis C
 PT virus, comprising at least one complementarily determining region of
 PT the variable domain of a human antibody -

XX Claim 3: Page 58; 64pp; English.

CC The present sequence represents the variable light chain of a human
 CC anti-hepatitis C virus (HCV) antibody. The sequence has been used to
 CC construct antibodies of the invention. These antibodies comprise at
 CC least one complementarity determining region (CDR) of the variable
 CC domain of a human antibody that specifically recognizes a
 CC conformation-dependent epitope of HCV glycoprotein E2 and is capable
 CC of precipitating covalently or non-covalently associated E2/E1
 CC complexes. The antibodies are useful for preventing (re)infection of
 CC HCV and are useful for eliminating HCV from a human or a human
 CC animal. The antibodies are useful for diagnosing chronic hepatitis C
 CC for the presence of neutralization of binding of HCV glycoprotein E2 on
 CC to tablet cells. The antibodies are useful for the treatment or
 CC prevention of HCV infection or recurrence of HCV infection, in which
 CC they are administered prior, during or after liver transplantation.
 CC In liver transplantation, the antibodies are also useful
 CC of infection of Tupaia-hepatocyte with HCV-infectious human sera.

XX Sequence 108 AA:

Query Match 81.6% Score 31: DB 21: Length 108:
 Best Local Similarity 71.4% Pred. No. 34:
 Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:
 OY 1 EDNORPS 7
 :||:||||
 Db 49 Kdnrps 55

Search completed: November 19, 2001, 08:12:36
 Job time: 89 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:23:16 ; Search time 526.89 seconds
(without alignments)
3.689 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EMDRPS 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 3148936 seps, 27755704 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 00

Maximum Match 1008

Listing file: # summaries

Database : Pending_Patents_AA_Main.*

- 1: /cgn2_6/prodata/2/paa/US06_COMB.pep.*
- 2: /cgn2_6/prodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/prodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 6: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 7: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 8: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 9: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 10: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 11: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 12: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 13: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 14: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
- 15: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 16: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 17: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 18: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 19: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 20: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 21: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 22: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 23: /cgn2_6/prodata/2/paa/US09_COMB.pep.*
- 24: /cgn2_6/prodata/2/paa/US09_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the predicted score. The
score is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	38	100.0	7	1	PCT-US00-18152-65	Sequence 65, Appl
2	38	100.0	7	20	US-09-610-118-65	Sequence 65, Appl
3	38	100.0	7	22	US-09-632-312-65	Sequence 65, Appl
4	38	100.0	79	24	US-60-163-062-790	Sequence 790, App
5	38	100.0	79	24	US-60-163-062-948	Sequence 948, App
6	38	100.0	88	24	US-60-165-053-2358	Sequence 2358, App
7	38	100.0	94	24	US-60-165-053-181	Sequence 181, App
8	38	100.0	94	24	US-60-165-053-181	Sequence 181, App
9	38	100.0	94	24	US-60-165-053-2359	Sequence 2359, App

10	38	100.0	94	24	US-60-234-446-712	Sequence 712, App
11	38	100.0	95	24	US-60-162-242-5385	Sequence 5385, App
12	38	100.0	100	24	US-60-196-710-4905	Sequence 4905, App
13	38	100.0	100	24	US-60-196-718-4971	Sequence 4971, App
14	38	100.0	104	24	US-60-162-247-3052	Sequence 3052, App
15	38	100.0	104	24	US-60-162-247-3052	Sequence 3052, App
16	38	100.0	108	24	US-60-169-840-7162	Sequence 7162, App
17	38	100.0	108	24	US-60-169-840-7162	Sequence 7162, App
18	38	100.0	109	24	US-60-162-247-3052	Sequence 3052, App
19	38	100.0	111	24	US-60-162-247-4435	Sequence 4435, App
20	38	100.0	111	24	US-60-162-247-4435	Sequence 4435, App
21	38	100.0	111	24	US-60-169-840-8023	Sequence 8023, App
22	38	100.0	111	24	US-60-169-840-8023	Sequence 8023, App
23	38	100.0	111	24	US-60-169-840-8023	Sequence 8023, App
24	38	100.0	161	21	PCT-US00-265248-6775	Sequence 6775, App
25	38	100.0	218	21	US-09-760-479-543	Sequence 543, App
26	38	100.0	258	1	PCT-US00-19110-1334	Sequence 1334, App
27	38	100.0	259	1	US-09-043-5228-13	Sequence 13, App
28	38	100.0	26	14	US-09-043-5228-13	Sequence 13, App
29	34	89.5	7	14	US-09-043-5228-13	Sequence 13, App
30	34	89.5	101	1	PCT-US01-10472-85	Sequence 85, App
31	34	89.5	109	14	US-09-043-5228-9	Sequence 9, App
32	34	89.5	109	14	US-09-043-5228-9	Sequence 9, App
33	34	89.5	110	14	US-09-043-5228-24	Sequence 24, App
34	34	89.5	110	14	US-09-043-5228-24	Sequence 24, App
35	34	89.5	114	23	US-09-043-5228-1194	Sequence 1194, App
36	34	89.5	114	23	US-09-043-5228-1194	Sequence 1194, App
37	34	89.5	117	21	US-09-760-479-771	Sequence 771, App
38	34	89.5	117	21	US-09-760-479-771	Sequence 771, App
39	34	89.5	233	24	US-60-222-372-1	Sequence 1, App
40	34	89.5	244	1	PCT-US01-19110-1842	Sequence 1842, App
41	34	89.5	244	22	US-09-880-748-1842	Sequence 1842, App
42	34	89.5	246	17	US-09-315-574-13	Sequence 13, App
43	34	89.5	246	17	US-09-315-574-13	Sequence 13, App
44	34	89.5	248	1	PCT-US01-19110-1273	Sequence 1273, App
45	33	86.8	248	22	US-09-880-748-1842	Sequence 1842, App

ALIGNMENTS

RESULT 1

PCT-US00-18152-65

Sequence 65, Application PCT/US00018152

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

TITLE OF INVENTION: GLYCOPROTEIN VI AND USUS THEREOF

FILE REFERENCE: 783, 811, 812 PCT/US00/18152

CURRENT FILING DATE: 2000-06-30

EARLIER FILING DATE: 2/14/00

EARLIER APPLICATION NUMBER: 09/503,387

EARLIER FILING DATE: 12/6/99

EARLIER APPLICATION NUMBER: 09/454,824

EARLIER FILING DATE: 07/0/99

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 65

LENGTH: 7

TYPE: PPT

ORGANISM: Homo sapiens

PCT-US00-18152-65

Query Match 100.0%; Score 38; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. 2.9e-06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMDRPS 7
DB 1 EMDRPS 7

LENGTH: 95
 TYPE: PRT
 ORGANISM: Human
 US-60-162-247-4885

Query Match
 Best Local Similarity 100.0%; Score 38; DB 24; Length 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORPS 7
 1111111
 DB 39 EDNORPS 45

RESULT 12
 US-60-162-247-4885
 Sequence 4885, Application US/60162247
 GENERAL INFORMATION:
 APPLICANT: Bionaz21, Vivien
 TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 TITLE OF INVENTION: ISOLATED ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 FILE REFERENCE: CLO00127
 CURRENT FILING DATE: 1999-10-29
 NUMBER OF SEQ ID NOS: 5442
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NOS: 1-5442
 LENGTH: 95
 TYPE: PRT
 ORGANISM: Human
 US-60-162-247-4885

Query Match
 Best Local Similarity 100.0%; Score 38; DB 24; Length 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORPS 7
 1111111
 DB 39 EDNORPS 45

RESULT 13
 US-60-196-710-4905
 Sequence 4905, Application US/60196710
 GENERAL INFORMATION:
 APPLICANT: Bionaz21, Vivien
 TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
 FILE REFERENCE: CLO00450
 CURRENT FILING DATE: 2000-04-13
 NUMBER OF SEQ ID NOS: 7166
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NOS: 1-7166
 LENGTH: 100
 TYPE: PRT
 ORGANISM: HUMAN
 US-60-196-710-4905

Query Match
 Best Local Similarity 100.0%; Score 38; DB 24; Length 100;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORPS 7
 1111111
 DB 73 EDNORPS 79

RESULT 14
 US-60-196-718-4971
 Sequence 4971, Application US/60196718
 GENERAL INFORMATION:
 APPLICANT: Bionaz21, Vivien
 TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 FILE REFERENCE: CLO00456
 CURRENT FILING DATE: 2000-04-13
 NUMBER OF SEQ ID NOS: 7494
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NOS: 1-7494
 LENGTH: 100
 TYPE: PRT
 ORGANISM: HUMAN
 US-60-196-718-4971

Query Match
 Best Local Similarity 100.0%; Score 38; DB 24; Length 100;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORPS 7
 1111111
 DB 73 EDNORPS 79

RESULT 15
 US-60-162-247-3052
 Sequence 3052, Application US/60162247
 GENERAL INFORMATION:
 APPLICANT: Bionaz21, Vivien
 TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 TITLE OF INVENTION: ISOLATED ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 FILE REFERENCE: CLO00127
 CURRENT FILING DATE: 1999-10-29
 NUMBER OF SEQ ID NOS: 5442
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NOS: 1-5442
 LENGTH: 104
 TYPE: PRT
 ORGANISM: Human
 US-60-162-247-3052

Query Match
 Best Local Similarity 100.0%; Score 38; DB 24; Length 104;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORPS 7
 1111111
 DB 51 EDNORPS 57

Search completed: November 19, 2001, 08:23:16
 Job Time: 729 sec

THIS PAGE BLANK (USPTO)

GenCore Version 4.5
Copyright (c) 1995 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:23:32 (without alignments)
3,259 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNORPS 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 25329 seqs, 5326477 residues

Total number of hits satisfying chosen parameters: 23229

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Pending Patents_AA.New:
1: /cgn2_6/prodata/1/paa/ECT_NEW.COMB.pep:*
2: /cgn2_6/prodata/1/paa/USO6_NEW.COMB.pep:*
3: /cgn2_6/prodata/1/paa/USO8_NEW.COMB.pep:*
4: /cgn2_6/prodata/1/paa/USO8_NEW.COMB.pep:*
5: /cgn2_6/prodata/1/paa/USO9_NEW.COMB.pep:*
6: /cgn2_6/prodata/1/paa/USO6_NEW.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	US-09-972-656-13	Sequence 13, App1
2	38	100.0	7	US-09-972-656-130	Sequence 130, App1
3	38	100.0	7	US-09-972-656-106	Sequence 106, App1
4	33	86.8	7	US-09-972-656-14	Sequence 14, App1
5	33	86.8	7	US-09-972-656-20	Sequence 20, App1
6	33	86.8	7	US-09-972-656-90	Sequence 90, App1
7	33	86.8	7	US-09-972-656-102	Sequence 102, App1
8	29	76.3	7	US-09-972-656-18	Sequence 18, App1
9	29	76.3	7	US-09-972-656-89	Sequence 89, App1
10	28	73.7	7	US-09-972-656-105	Sequence 105, App1
11	28	73.7	7	US-09-972-656-146	Sequence 146, App1
12	28	73.7	7	US-09-972-656-106	Sequence 106, App1
13	28	73.7	7	US-09-972-656-118	Sequence 118, App1
14	27	71.1	7	US-09-972-656-119	Sequence 119, App1
15	27	71.1	7	US-09-972-656-124	Sequence 124, App1
16	27	71.1	7	US-09-972-656-134	Sequence 134, App1
17	27	71.1	7	US-09-972-656-135	Sequence 135, App1
18	27	71.1	7	US-09-972-656-136	Sequence 136, App1
19	27	71.1	7	US-09-972-656-137	Sequence 137, App1
20	27	71.1	7	US-09-972-656-138	Sequence 138, App1
21	27	71.1	7	US-09-972-656-139	Sequence 139, App1
22	27	71.1	7	US-09-972-656-140	Sequence 140, App1
23	26	68.4	7	US-09-972-656-141	Sequence 141, App1
24	26	68.4	7	US-09-972-656-142	Sequence 142, App1
25	26	68.4	7	US-09-972-656-143	Sequence 143, App1
26	26	68.4	7	US-09-972-656-144	Sequence 144, App1
27	26	68.4	7	US-09-972-656-145	Sequence 145, App1

28	26	68.4	496	5	US-09-815-242-12203	Sequence 12203, A
29	26	68.4	744	5	US-09-815-242-13390	Sequence 13390, A
30	26	68.4	850	1	PCT-US01-07265-4	Sequence 4, App1
31	26	68.4	904	5	US-09-972-656-146	Sequence 146, App1
32	26	68.4	904	5	US-09-972-656-147	Sequence 147, App1
33	26	68.4	909	5	US-09-972-656-124	Sequence 124, App1
34	26	68.4	984	5	US-09-972-656-127	Sequence 127, App1
35	25	65.8	7	5	US-09-972-656-17	Sequence 17, App1
36	25	65.8	148	5	US-09-972-656-18	Sequence 18, App1
37	25	65.8	148	5	US-09-970-711-18	Sequence 18, App1
38	25	65.8	133	5	US-09-897-516-8284	Sequence 8284, App1
39	25	65.8	133	5	US-09-897-516-8284	Sequence 8284, App1
40	25	65.8	212	5	US-09-972-656-99	Sequence 99, App1
41	25	65.8	214	5	US-09-972-656-96	Sequence 96, App1
42	25	65.8	234	5	US-09-576-424-2	Sequence 2, App1
43	25	65.8	268	1	PCT-US01-11857-1	Sequence 1, App1
44	25	65.8	268	5	US-09-976-118-1	Sequence 1, App1
45	25	65.8	300	5	US-09-897-516-4820	Sequence 4820, App1

ALIGNMENTS

RESULT 1	US-09-972-656-13	US-09-972-656-13
Sequence 13, Application US/09972656	Sequence 130, Application US/09972656	Sequence 130, Application US/09972656
APPLICANT: Deshpande, Rajendra	APPLICANT: Deshpande, Rajendra	APPLICANT: Deshpande, Rajendra
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma	TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma	TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
FILE REFERENCE: A-799	FILE REFERENCE: A-799	FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972.656	CURRENT APPLICATION NUMBER: US/09/972.656	CURRENT APPLICATION NUMBER: US/09/972.656
NUMBER OF SEQ NOS: 135	NUMBER OF SEQ NOS: 135	NUMBER OF SEQ NOS: 135
SOFTWARE: PatentIn version 3.0	SOFTWARE: PatentIn version 3.0	SOFTWARE: PatentIn version 3.0
SEQ ID NO 13	SEQ ID NO 13	SEQ ID NO 13
LENGTH: 7	LENGTH: 7	LENGTH: 7
TYPE: PRT	TYPE: PRT	TYPE: PRT
ORGANISM: Homo sapiens	ORGANISM: Homo sapiens	ORGANISM: Homo sapiens
US-09-972-656-13	US-09-972-656-13	US-09-972-656-13
Query Match	100.0%	Score 38: DB 5: Length 7:
Best Local Similarity	100.0%	Pred. No. 2.2e+04:
Matches 7: Conservative	0: Mismatches	0: Indels
0: Gaps	0: Gaps	0: Gaps
Db	1 EDNORPS 7	1 EDNORPS 7
Qy	1 EDNORPS 7	1 EDNORPS 7
RESULT 2	US-09-972-656-130	US-09-972-656-130
Sequence 130, Application US/09972656	Sequence 130, Application US/09972656	Sequence 130, Application US/09972656
APPLICANT: Deshpande, Rajendra	APPLICANT: Deshpande, Rajendra	APPLICANT: Deshpande, Rajendra
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma	TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma	TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
FILE REFERENCE: A-799	FILE REFERENCE: A-799	FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972.656	CURRENT APPLICATION NUMBER: US/09/972.656	CURRENT APPLICATION NUMBER: US/09/972.656
NUMBER OF SEQ NOS: 135	NUMBER OF SEQ NOS: 135	NUMBER OF SEQ NOS: 135
SOFTWARE: PatentIn version 3.0	SOFTWARE: PatentIn version 3.0	SOFTWARE: PatentIn version 3.0
SEQ ID NO 130	SEQ ID NO 130	SEQ ID NO 130
LENGTH: 103	LENGTH: 103	LENGTH: 103
TYPE: PRT	TYPE: PRT	TYPE: PRT
ORGANISM: Homo sapiens	ORGANISM: Homo sapiens	ORGANISM: Homo sapiens
FEATURE: Misc.	FEATURE: Misc.	FEATURE: Misc.
NAME/KEY: (7)-(7)	NAME/KEY: (7)-(7)	NAME/KEY: (7)-(7)
LOCATION: (7)-(7)	LOCATION: (7)-(7)	LOCATION: (7)-(7)
OTHER INFORMATION: Unidentified	OTHER INFORMATION: Unidentified	OTHER INFORMATION: Unidentified

```

; NAME/KEY: Misc.
; LOCATION: (33)..(33)
; OTHER INFORMATION: Unidentified
; NAME/KEY: Misc.
; LOCATION: (34)..(34)
; OTHER INFORMATION: Unidentified
; NAME/KEY: Misc.
; LOCATION: (35)..(35)
; OTHER INFORMATION: Unidentified
; NAME/KEY: Misc.
; LOCATION: (36)..(36)
; OTHER INFORMATION: Unidentified
US-09-972-656-130

```

```

Query Match          100.0%; Score 38; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 EDNORS 7
    11:11111
    56 EDNORS 62

```

```

RESULT 3
US-09-972-656-108
; Sequence 108, Application US/09972656
; GENERAL INFORMATION:
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972.656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-108

```

```

Query Match          100.0%; Score 38; DB 5; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 EDNORS 7
    11:11111
    51 EDNORS 57

```

```

RESULT 4
US-09-972-656-14
; Sequence 14, Application US/09972656
; GENERAL INFORMATION:
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972.656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-14

```

```

Query Match          86.8%; Score 33; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.2e-04;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 EDNORS 7
    11:11111
    1 EDNORS 7

```

```

RESULT 5
US-09-972-656-20
; Sequence 20, Application US/09972656
; GENERAL INFORMATION:
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972.656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-20

```

```

Query Match          86.8%; Score 33; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.2e-04;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 EDNORS 7
    11:11111
    1 EDNORS 7

```

```

RESULT 6
US-09-972-656-90
; Sequence 90, Application US/09972656
; GENERAL INFORMATION:
; APPLICANT: Desjardine, Rajendra
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972.656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-90

```

```

Query Match          86.8%; Score 33; DB 5; Length 216;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 EDNORS 7
    11:11111
    51 EDNORS 57

```

```

RESULT 7
US-09-972-656-102
; Sequence 102, Application US/09972656
; GENERAL INFORMATION:
; APPLICANT: Desjardine, Rajendra
; APPLICANT: Tsai, Mei-Mei

```

```

: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: TITLE OF INVENTION: Neutralizing Activity
: FILE REFERENCE: A-799
: CURRENT APPLICATION NUMBER: US/09/972.656
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: Patentin version 3.0
: SEQ ID NO: 1
: LENGTH: 218
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-972-656-102

```

```

Query Match
Best Local Similarity: 86.38; Score 33; DB 5; Length 218;
Matches: 6; Conservative 1; Mismatches 0; Gaps 0;

```

```

Qy      1 EDNRPS 7
Db      51 EDNRPS 57

```

```

RESULT 8
: Sequence 12, Application US/09972656
: GENERAL INFORMATION:
: APPLICANT: Deshpande, Rajendra
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: FILE REFERENCE: A-799 Neutralizing Activity
: CURRENT APPLICATION NUMBER: US/09/972.656
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: Patentin version 3.0
: SEQ ID NO: 12
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-972-656-12

```

```

Query Match
Best Local Similarity: 76.38; Score 29; DB 5; Length 7;
Matches: 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 EDNRPS 7
Db      1 EDNRPS 7

```

```

RESULT 9
: Sequence 88, Application US/09972656
: GENERAL INFORMATION:
: APPLICANT: Deshpande, Rajendra
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: FILE REFERENCE: A-799 Neutralizing Activity
: CURRENT APPLICATION NUMBER: US/09/972.656
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: Patentin version 3.0
: SEQ ID NO: 88
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-972-656-88

```

```

Query Match      76.38; Score 29; DB 5; Length 217;

```

```

Best Local Similarity: 71.48; Pred. No. 7.6;
Matches: 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 EDNRPS 7
Db      51 EDNRPS 57

```

```

RESULT 10
: Sequence 516, Application US/09897516
: GENERAL INFORMATION:
: APPLICANT: Corbido, David R.
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Huesing, Joseph E.
: APPLICANT: Krasomil-Osterfeld, Karina C.
: APPLICANT: Malvar, Thomas M.
: APPLICANT: Miller, Steven C.
: APPLICANT: Spillmann, David L.
: TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
: FILE REFERENCE: 38-21(51847)B
: CURRENT APPLICATION NUMBER: US/09/897.516
: CURRENT FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: 60/215, 161
: PRIOR FILING DATE: 2000-06-30
: NUMBER OF SEQ ID NOS: 8409
: SEQ ID NO: 5795
: LENGTH: 176
: TYPE: PRT
: ORGANISM: Xenorhabdus sp.
US-09-897-516-5795

```

```

Query Match
Best Local Similarity: 73.78; Score 28; DB 5; Length 176;
Matches: 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EDNRPS 7
Db      116 EDNRPS 122

```

```

RESULT 11
: Sequence 5706, Application US/09815242
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Huesing, Joseph E.
: APPLICANT: Zwick, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trewick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815.242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191, 078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206, 848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207, 727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242, 578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253, 625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257, 931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269, 308

```

```

? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 5706
? LENGTH: 305
? TYPE: PRF
? ORGANISM: Staphylococcus aureus
US-09-615-242-5706

```

```

Query Match      73.7%: Score 28; DB 5; Length 305;
Best Local Similarity 66.7%: Pred. No. 18;
Matches 4; Conservative 2; Mismatches 0; Gaps 0;

```

```

OY      1 EDNORP 6
DB      15 EDNORP 20

```

```

RESULT 12
US-09-615-242-12466
? Sequence 12466, Application US/09815242
? ORGANISM: Staphylococcus aureus
? APPLICANT: Haselbeck, Robert
? APPLICANT: Ohlsson, Karl L.
? APPLICANT: Zykand, Judith W.
? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John D.
? APPLICANT: Carr, Grant J.
? APPLICANT: Krasomil-Osterfeld, Karina C.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? FILE REFERENCE: ELITRA.011A
? CURRENT FILING DATE: 2001-03-21
? PRIOR FILING DATE: 2000-03-21, 078
? PRIOR FILING DATE: 2000-03-21, 078
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2001-02-16
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 12466
? LENGTH: 347
? TYPE: PRF
? ORGANISM: Staphylococcus aureus
US-09-815-242-12466

```

```

Query Match      73.7%: Score 28; DB 5; Length 347;
Best Local Similarity 66.7%: Pred. No. 20;
Matches 4; Conservative 2; Mismatches 0; Gaps 0;

```

```

OY      1 EDNORP 6
DB      15 EDNORP 20

```

```

RESULT 13
US-09-815-242-5118
? Sequence 5118, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert

```

```

? APPLICANT: Ohlsson, Karl L.
? APPLICANT: Zykand, Judith W.
? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John D.
? APPLICANT: Carr, Grant J.
? APPLICANT: Yamamoto, Robert T.
? APPLICANT: Krasomil-Osterfeld, Karina C.
? APPLICANT: Xue, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? FILE REFERENCE: ELITRA.011A
? CURRENT APPLICATION NUMBER: US/09/815,242
? CURRENT FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-03-21, 078
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2001-02-16
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 5118
? LENGTH: 1317
? TYPE: PRF
? ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5118

```

```

Query Match      73.7%: Score 28; DB 5; Length 1317;
Best Local Similarity 71.4%: Pred. No. 81;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

```

```

OY      1 EDNORPS 7
DB      831 DDNORPS 837

```

```

RESULT 14
US-09-897-516-7544
? Sequence 7544, Application US/09897516
? GENERAL INFORMATION:
? APPLICANT: Corbin, David R.
? APPLICANT: Goldman, Barry S.
? APPLICANT: Haselbeck, Robert T.
? APPLICANT: Haselberg, Joseph B.
? APPLICANT: Krasomil-Osterfeld, Karina C.
? APPLICANT: Malvar, Steven M.
? APPLICANT: Slater, Steven C.
? APPLICANT: Spiridonov, Sergei
? TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
? FILE REFERENCE: US/09/897,516
? CURRENT APPLICATION NUMBER: US/09/897,516
? CURRENT FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: US 60/215, 161
? PRIOR FILING DATE: 2000-06-30
? NUMBER OF SEQ ID NOS: 8409
? SEQ ID NO 7544
? LENGTH: 246
? TYPE: PRF
? ORGANISM: Xenorhabdus sp.
US-09-897-516-7544

```

```

Query Match      71.1%: Score 27; DB 5; Length 246;
Best Local Similarity 81.3%: Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Gaps 0;

```

OY 2 DNORGES 7
 111 11
 Db 233 DNORGES 238

RESULT 15
 US-09-615-242-11924

GENERAL INFORMATION: US-09-615-242-11924 Application US/09015242

APPLICANT: Haselmeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Carf, Grant J.

APPLICANT: Trowick, John D.

APPLICANT: Harnwood, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21,078

PRIOR APPLICATION NUMBER: 60/291,078

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

NUMBER OF SEQ ID NOS: 14110

SEQ ID NO 11544

LENGTH: 314

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-615-242-11924

Search completed: November 19, 2001, 08:23:32
 Job time: 744 sec

Query Match 71 1%; Score 27; DB 5; Length 314;
 Best Local Similarity: 83 3%; Prev 30;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDNGRP 6
 11111
 Db 63 EDNGRP 68

THIS PAGE BLANK (USPTO)


```

: INFORMATION FOR SEQ ID NO: 16:
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 106 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
US-08-259-372A-16

```

Query Match	89.58;	Score 34;	DB 1;	Length 106;
07.7A				

Qy	1	EDNQPS	7
Db	49	EDNKRPS	55

RESULT# 2
US-08-468-671-16
Sequence 16: Application US/09468671
Patent No. 564077
GENERAL INFORMATION:
APPLICANT: Osberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Osberg and Norstrand and Gray LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MONITOR TYPE: COPY FILE
MONITOR TYPE: INCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIORITY DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 11-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
ADDRESS/DOCKET NUMBER: 10123-50-7
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids

```

;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-468-671-16

```

```

Query Match      89.5%; Score 34; DB 1; Length 106
Best Local Similarity 85.7%; Pred. No. 4;
Matches 6; Conservative 1; Mismatches 0; Indels

```

QY	1	EDNRPS	7
		:	
Db	49	EDNKRPS	55

```

1      RESULT 3
2      US-08-665-402-39
3      Sequence 39, Application US/08665202
4      INVENTION NO. 59732261
5      GENERAL INFORMATION:
6      APPLICANT: Marks, James D.
7      INVENTOR: Schlier, Robert
8      TITLE OF INVENTION: No. 59732261 High Affinity Human Antibodies to
9      Tumor Antigens
10     TITLE OF INVENTION: Tumor Antigens
11     NUMBER OF SEQUENCES: 141
12     NUMBER OF SEQUENCES: 141
13     ADDRESS: Townsend and Townsend and Crew LLP
14     STREET: Two Embarcadero Center, Eighth Floor
15     CITY: San Francisco
16     STATE: California
17     COUNTRY: USA834
18     PUBLICATION NO. 2008/065202
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: PatentIn Release #1.0, Version #1.30
24     CURRENT APPLICATION DATA: 08/665.202
25     FILING DATE: 10-13-JUN-1996
26     CLASSIFICATION: 424
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER: US 60/000.238
29     FILING DATE: 14-JUN-1995
30     PRIOR APPLICATION DATA: US 60/000.250
31     APPLICATION NUMBER: US 60/000.250
32     FILING DATE: 15-JUN-1995
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Hunter, Tom
35     REGISTRATION NUMBER: 38,498
36     REFERENCE/DOCKET NUMBER: 0230/E-061410
37     TELEPHONE: (415) 576-0200
38     TELEPHONE: (415) 576-0200
39     TELEFAX: (415) 576-0300
40     INFORMATION FOR SEQ ID NO: 39:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 112 amino acids
43     TYPE: amino acid
44     STRANDEDNESS: single
45     TOPOLOGICAL: linear
46     MOLECULE TYPE: peptide
47     US-08-665-202-39

```

Query Match	86.8%;	Score 33;	DB 2;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 6.7;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

Qy	2	DNQRP	7
Db	52	DNQRP	57

RESULT 4
US-08-259-372A-10
SEQUENCE 19, Application US/08259372A
Patent No. 5565154
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Ostberg, Lars G. and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 11-OCT-1986
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELEPHONE: (415) 576-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-259-372A-10

Query Match 84.2% Score 32, DB 1, Length 108,
Best Local Similarity 71.4% Pctd. No. 10;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDWARDS 7
Db 49 DDMERPS 55

RESULT 5
US-08-468-671-10
SEQUENCE 19, Application US/08468671
Patent No. 5648077
GENERAL INFORMATION:

APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Ostberg, Lars G. and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-671-10

Query Match 84.2% Score 32, DB 1, Length 108,
Best Local Similarity 71.4% Pctd. No. 10;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDWARDS 7
Db 49 DDMERPS 55

RESULT 6
US-08-765-1798-19
SEQUENCE 19, Application US/087651798
Patent No. 5854027
GENERAL INFORMATION:
APPLICANT: STEINBE, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-875-9448-5

Query Match 78.9% Score 30; DB 3; Length 462;
Best Local Similarity 83.3% Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DNORPS 7
DB 412 DNORPA 417

RESULT 12
US-09-116-049-4
Sequence 4; Application US/09116049A
Patent No. 6248351
GENERAL INFORMATION:
APPLICANT: Hung, Men-Chie
TITLE OF INVENTION: HUMAN PEAS IS A TUMOR SUPPRESSOR FOR CANCER CELLS
CURRENT APPLICATION NUMBER: US/09/116.049A
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
TITLE OF INVENTION: HUMAN PEAS IS A TUMOR SUPPRESSOR
REFERENCE/DOCKET NUMBER: US/09-116-049-4
CORRESPONDENCE ADDRESS:
ADDRESSER: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDICIN TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780.835B
PRIORITY NUMBER: 1997-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Milson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UTSC500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-5000

Query Match 78.9% Score 30; DB 4; Length 462;
Best Local Similarity 83.3% Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DNORPS 7
DB 412 DNORPA 417

RESULT 13
US-08-780-835B-2
Sequence 2; Application US/08780835B
Patent No. 5922688
GENERAL INFORMATION:
APPLICANT: Hung, Mien-Chie
TITLE OF INVENTION: PEAS IS A Tumor Suppressor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780.835B
PRIORITY NUMBER: 1997-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Milson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UTSC500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-5000

TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-780-835B-2

Query Match 78.9% Score 30; DB 2; Length 555;
Best Local Similarity 83.3% Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DNORPS 7
DB 505 DNORPA 510

RESULT 14
US-09-303-268-2
Sequence 2; Application US/09303268
Patent No. 6172212
GENERAL INFORMATION:
APPLICANT: Hung, Mien-Chie
TITLE OF INVENTION: PEAS IS A Tumor Suppressor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303.268
PRIORITY NUMBER: 1997-1997
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780.835
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Milson, Mark B. 37,259
REFERENCE/DOCKET NUMBER: UTSC500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-303-268-2

Query Match 78.9% Score 30; DB 4; Length 555;
Best Local Similarity 83.3% Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DNORPS 7
DB 505 DNORPA 510

```

RESULT 15
US-09-116-049-2
Sequence 2 Application US/0916049A
Patent No. 6248351
GENERAL INFORMATION:
APPLICANT: Hung, Men-Chie
TITLE OF INVENTION: HUMAN PEN3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
FILE REFERENCE: US-582
PUBLICATION NUMBER: US/09/116,049A
CURRENT PUBLICATION NO. 18-07-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 555
TYPE: PRT
ORIGIN: MUS
US-09-116-049-2 Mus musculus

```

```

Query Match 78.9% Score 30; DB 4; Length 555;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 DNORPS 7
|||||
Db 505 DNORPA 510

```

Search completed: November 19, 2001, 08:13:26
 Job time: 139 sec

THIS PAGE BLANK (USPTO)

A:Cross-references: GDB:119342; OMIM:147240
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-59/Domain: Immunoglobulin homology <IMH>
 F:1-59/Region: framework 1
 F:2-89/Disulfide bonds: status predicted

Query Match 89.5%; Score 34; DB 1; Length 109;
 Best Local Similarity 85.7%; Pred. No. 2.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORP 7
 DB 51 EDNORP 57

RESULT 3
 L:IMMUNoglobulin chain V-1 region (New) - human
 C:Species: Homo sapiens (man)
 C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 24-Nov-1999
 C:Accession: A01964
 R:Langier, B.; Steinmetz-Kayne, M.; Hilschmann, N.; Hoppe-Seyler, A. Z. Physiol. Chem. 349: 945-951, 1968
 A>Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subg
 A:Accession: A01964
 A:Residue type: protein
 A:Residues: 1-111 <LAN>
 C:Comment: This is a Bence Jones protein.
 C:Genetics:
 A:Gene: GDB:IGLV6
 A:Map position: 22q11.2-22q11.2
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: blocked amino end; heterotrimer
 F:1-91/Domain: Immunoglobulin homology <IMH>
 F:1-91/Region: framework 1
 F:22-89/Disulfide bonds: status predicted (probably pyrrolidone carboxylic acid) #statu

Query Match 89.5%; Score 34; DB 1; Length 111;
 Best Local Similarity 85.7%; Pred. No. 2.8;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORP 7
 DB 51 EDNORP 57

RESULT 4
 L:IMMUNoglobulin chain precursor V-Y1 region (BB4) - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
 C:Accession: A01990
 R:Anderson, M.L.M.; Brown, L.; McKenzie, E.; Kellow, J.E.; Young, B.D.
 A>Title: Cloning and sequence analysis of an Ig lambda light chain mRNA expressed in the
 A:Accession: A01990
 A:Molecule type: mRNA
 A:Residues: 1-131 <AND>
 C:Genetics:
 A:Gene: GDB:IGLVE
 A:Cross-references: GDB:119342; OMIM:147240

A:Map position: 22q11.2-22q11.2
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Domain: signal sequence; heterotrimer predicted <SIG>
 F:20-41/Region: framework 1
 F:34-112/Domain: immunoglobulin chain V-Y1 region (BB4) #status predicted <IMH>
 F:55-69/Region: framework 2
 F:70-76/Region: complementarity-determining 2
 F:77-110/Region: framework 3 partially determining 3
 F:110-117/Region: framework 4
 F:41-110/Disulfide bonds: status predicted

Query Match 89.5%; Score 34; DB 1; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORP 6
 DB 70 EDNORP 75

RESULT 5
 L:IMMUNoglobulin chain B223_F2_77 - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
 C:Accession: S72947
 R:Smith, D.R.; Robinson, K.
 A:Submitted to the EMBL Data Library November 1993
 A:Reference number: S72587
 A:Accession: S72947
 A:Reference number: S72587
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-266 <SM>
 A:Cross-references: EMBL:U00019; NID:g467079; PDB:1AA17283.1; PDB:g467100

Query Match 89.5%; Score 34; DB 2; Length 266;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNORP 6
 DB 103 EDNORP 108

RESULT 6
 L:IMMUNoglobulin chain A2G23590 (Imported) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001
 C:Accession: T02558; A84735
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke
 A:Submitted to the EMBL Data Library July 1998
 A:Reference number: Z14678
 A:Accession: T02558
 A:Reference number: Z14678
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-704 <ROD>
 A:Cross-references: EMBL:AC004681; NID:g3298532; PDB:g3298547
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, T.P.; Bentol, M.I.; Tomo, C.D.; Fujii, C.Y.; Koo, H.; Medici, C.S.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

RESULT 10
R70690
Hypothetical protein F10B5.3 - *Caenorhabditis elegans*
C. elegans, *Caenorhabditis elegans*
S.C. Specter, C. O'Connell, J. R. Eickholt, D. L. Spector
J. Mol. Biol. 270:1-12 (1998) *Accession: R70690
R1:Sime, M.
Submitted to the EMBL Data Library, February 1995
Reference number: Z19310

RESULT 15
 A45710
 BRRP2 gene homolog - bovine herpesvirus 4 (fragment)
 C:Species: bovine herpesvirus 4
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #exl_change 08-Oct-1999
 C:Accession: A45710
 J:Virus: Herpesvirus 1, 17-184, 1993
 J:Virus: Herpesvirus 1, 17-184, 1993
 A:Title: Characterization of a bovine herpesvirus 4 immediate-early RNA encoding a homolog
 A:Reference number: A45710; MUID:93124571
 A:Accession: A45710
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Molecule type: Nucleic acid
 A:Accession: A45710
 A:Cross-reference: MUID:93124571; PTD:AAA46056.1; PTD:9330763
 A:Note: sequence extracted from NCBI database (NCBI:122331, NCBI:122333)

Query Match 78.9%; Score 30; DB 2; Length 332;
 Best Local Similarity 83.3%; Pred. No. 63;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EBNORP 6
 I:||||
 DB 11 EBNORP 16

Search completed: November 19, 2001, 08:14:23
 Job time: 196 sec

THIS PAGE BLANK (USPTO)

GenScope version 4.5
Copyright (c) 1995 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:25:35 ; Search time 27.32 Seconds

(without alignments)
8.777 Million cell updates/sec

Title: US-09-610-118-65

Perfect score: 38

Sequence: 1 EDNORPS 7

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_39*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	112	1 LV16_HUMAN	P01721 homo sapien
2	34	89.5	109	1 LV16_HUMAN	P04208 homo sapien
3	34	89.5	111	1 LV16_HUMAN	P01319 homo sapien
4	33	89.5	111	1 LV16_HUMAN	P05318 homo sapien
5	33	86.8	111	1 LV16_HUMAN	P05318 homo sapien
6	32	84.2	111	1 LV16_HUMAN	P05318 homo sapien
7	32	84.2	460	1 VS41_CACEL	P00370 homo sapien
8	30	78.9	108	1 LV58_HUMAN	P01719 homo sapien
9	30	78.9	332	1 V1E2_HSV4	O02484 bovine hearp
10	30	78.9	332	1 V1E2_HSV4	P75804 escherichia
11	30	78.9	332	1 V1E2_HSV4	P43268 mus sapien
12	30	78.9	554	1 SV1A_HUMAN	P43268 mus sapien
13	30	78.9	620	1 ITRK_MOUSE	P09867 mus sapien
14	29	76.3	195	1 RO1L_BOVIN	P15200 rabies viru
15	29	76.3	202	1 VMA1_RABVA	P15200 rabies viru
16	29	76.3	202	1 VMA1_RABVA	P15200 rabies viru
17	29	76.3	202	1 VMA1_RABVA	P15200 rabies viru
18	29	76.3	202	1 VMA1_RABVA	P15200 rabies viru
19	29	76.3	202	1 VMA1_RABVA	P15200 rabies viru
20	29	76.3	318	1 RO1L_MOUSE	P04266 rabies viru
21	29	76.3	319	1 RO1L_MOUSE	P04266 rabies viru
22	29	76.3	319	1 RO1L_MOUSE	P04266 rabies viru
23	29	76.3	319	1 RO1L_MOUSE	P04266 rabies viru
24	29	76.3	319	1 RO1L_MOUSE	P04266 rabies viru
25	29	76.3	319	1 RO1L_MOUSE	P04266 rabies viru
26	29	76.3	319	1 RO1L_MOUSE	P04266 rabies viru
27	29	76.3	477	1 PR1G_HUMAN	P00162 etwalia chr
28	29	76.3	477	1 PR1G_HUMAN	P00162 etwalia chr
29	29	76.3	510	1 RRM_HUMAN	P05059 mus sapien
30	29	76.3	578	1 YDVG_SCHPO	O14266 schizosach
31	29	76.3	871	1 SYA_JADPY	O14266 schizosach
32	29	76.3	924	1 ORC1_DROME	O16810 drosophila
33	29	76.3	1140	1 RAL1_SCHMO	P33692 sorghum b1c

34	29	76.3	1193	1 DPO1_ADPO4	P87693 human adeno
35	29	76.3	1239	1 V120_EBV	P03189 homo sapien
36	29	76.3	1682	1 C1N6_HUMAN	O01118 human rhino
37	29	76.3	2164	1 POL2_HRV89	P07210 human rhino
38	28	73.7	78	1 V1S1_EPMO2	O22002 mycobacteri
39	28	73.7	107	1 LV1C_HUMAN	P01717 homo sapien
40	28	73.7	107	1 LV1C_HUMAN	P01717 homo sapien
41	28	73.7	449	1 RSN_ECOLI	P31061 escherichia
42	28	73.7	449	1 RSN_ECOLI	P31061 escherichia
43	28	73.7	449	1 RSN_ECOLI	P31061 escherichia
44	28	73.7	486	1 UNP1_CANAL	P22632 plasmodium
45	28	73.7	817	1 VAPL_YEAST	P37370 saccharomyc

ALIGNMENTS

RESULT 1
ID LV16_HUMAN STANDARD: PRT; 112 AA.

DT 21-JUL-1986 (rel. 01, Created)

DT 21-JUL-1986 (rel. 01, Last sequence update)

DT 15-JUL-1999 (rel. 38, Last annotation update)

ID LAMBDA CHAIN V-VI REGION AR.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Eumetazoa; Cnidaria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxId=9606;

RP SEQUENCE (AMYLLOID PROTEIN AR).

RX MEDLINE-82051000; PubMed-6797401;

RA Stetten K., Natvig J.B., Husby G., Junil J.;

RT "The complete amino acid sequence of a proteolytic

fragment of amyloid fibril protein Ar."

RL Biochem J 195; 195: 721-725

CC -1 MISCELLANEOUS; ABOUT HALF OF THE LAMBDA CHAIN C REGION IS MISSING

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

CC -1 MISCELLANEOUS; THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A

Query Match 92.1% Score 35, DB 1; Length 112;

Best Local Similarity 85.7% Pred No. 0.55;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNORPS 7

DB 51 EDNORPS 57

RESULT 2

ID LV16_HUMAN STANDARD: PRT; 109 AA.

DT 20-MAR-1987 (rel. 04, Created)

DT 20-MAR-1987 (rel. 04, Last sequence update)

DT 15-JUL-1999 (rel. 38, Last annotation update)

ID LAMBDA CHAIN V-VI REGION AR.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Eumetazoa; Cnidaria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxId=9606;

RP SEQUENCE

RX MEDLINE-83221661; PubMed-6407018;

RA Takahashi Y., Takahashi N., Tetsert D., Putnam F.W.:
 RT Complete covalent structure of a human immunoglobulin D: sequence of
 RL the heavy chain variable region. In: Immunoglobulin D: Molecular Biology
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
 DR PIR: A01967; L1HUMA.
 DR InterPro: IP8003006; *
 KW Pfam: PF00047; 19: 1.
 DR Immunoglobulin V region.
 FT DOMAIN 98 109 V SEGMENT
 FT DISULFID 22 89 J SEGMENT
 FT NON-TER 109 109 BY SIMILARITY.
 SO SEQUENCE 109 AA: B17856A8DF9BAC CRC64:
 Query Match 89.5% Score 34; DB 1; Length 109;
 Best Local Similarity 85.7% Pred. No. 0.89;
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;
 Indels 0; Caps 0;
 QY 1 EDNORPS 7
 DB 51 EDNORPS 57
 |||||
 RESULT 3
 ID LVIC_HUMAN STANDARD; PRT; 111 AA.
 AC P01701;
 DT 21-JUL-1986 (Rel. 01; Created)
 DT 21-JUL-1986 (Rel. 01; Last sequence update)
 DE 15-JUL-1999 (Rel. 38; Last annotation update)
 IG LAMBDA CHAIN V-I REGION NEW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC NCBI_TaxID=9606;
 RX MEDLINE=69060892; PubMed=4177823;
 RA Langer B., Steinmetz-Kayne M., Hilschmann N.:
 RT "The complete amino acid sequence of Bence Jones protein New (lambda-
 RT type). Subgroups in the variable part of immunoglobulin L-chains of
 RT the lambda-type." Physiol. Chem. 349:945-951(1966).
 CC -HYPERICAMBOUS; THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01964; L1HUM.
 DR HSSP: P01703; 7FAB.
 DR InterPro: IP8003006; *
 KW Pfam: PF00047; 19: 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 98 109 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 89 BY SIMILARITY.
 FT NON-TER 111 111
 SO SEQUENCE 111 AA: 11453 MW: AAEBCA3CA9F2AD3 CRC64:
 Query Match 89.5% Score 34; DB 1; Length 111;
 Best Local Similarity 85.7% Pred. No. 0.91;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNORPS 7
 DB 51 EDNORPS 57
 |||||
 RESULT 4
 ID LV6E_HUMAN STANDARD; PRT; 131 AA.
 AC P06319;
 DT 01-JAN-1988 (Rel. 06; Created)
 DT 01-JAN-1988 (Rel. 06; Last sequence update)
 DE 15-JUL-1999 (Rel. 38; Last annotation update)
 IG LAMBDA CHAIN V-VI REGION EBA PRECURSOR.
 SO SEQUENCE 131 AA: 11966 MW: 0C88B2F37CE24F CRC64:

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC NCBI_TaxID=9606;
 RX MEDLINE=3923440;
 RA Adelson-Miller L., Brown L., McKenzie E., Kellom J.E., Young B.D.:
 RT "Cloning and sequence analysis of an Ig lambda 19tc chain mRNA
 RT expressed in the Burkitt's lymphoma cell line EBA.*"
 RL Nucleic Acids Res. 13:2931-2941(1985).
 DR PIR: A01990; L6DUEB.
 DR HSSP: P01701; IP8003006; *
 KW Pfam: PF00047; 19: 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 131 IG LAMBDA CHAIN V-VI REGION EBA.
 FT DOMAIN 20 41 FRAMEWORK 1.
 FT DOMAIN 41 69 FRAMEWORK 2.
 FT DOMAIN 69 76 FRAMEWORK 3.
 FT DOMAIN 76 110 FRAMEWORK 4.
 FT DOMAIN 110 131 FRAMEWORK 5.
 FT DISULFID 131 131 BY SIMILARITY.
 FT NON-TER 131 131
 SO SEQUENCE 131 AA: 11447 MW: 02A3J79C8C05C2CD CRC64:
 Query Match 89.5% Score 34; DB 1; Length 131;
 Best Local Similarity 100.0% Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNORP 5
 DB 70 EDNORP 75
 |||||
 RESULT 5
 ID LV6D_HUMAN STANDARD; PRT; 111 AA.
 AC P06318;
 DT 01-JAN-1988 (Rel. 06; Created)
 DT 01-JAN-1988 (Rel. 06; Last sequence update)
 DE 15-JUL-1999 (Rel. 38; Last annotation update)
 IG LAMBDA CHAIN V-VI REGION WLT.
 CC -HYPERICAMBOUS; THIS IS A BENCE-JONES PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NC NCBI_TaxID=9606;
 RX MEDLINE=86122667; PubMed=4080539;
 RA Langer B., Steinmetz-Kayne M., Hilschmann N.:
 RT "The complete amino acid sequence of a lambda VI primary (VL) amyloid protein
 RT (WLT).".
 RL Scand. J. Immunol. 22:653-660(1985).
 DR PIR: A01989; L6HULF.
 DR HSSP: P01709; 2MGS.
 DR InterPro: IP8003006; *
 KW Pfam: PF00047; 19: 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 22
 FT DOMAIN 23 35 FRAMEWORK 1.
 FT DOMAIN 36 50 FRAMEWORK 2.
 FT DOMAIN 51 57 FRAMEWORK 3.
 FT DOMAIN 58 101 FRAMEWORK 4.
 FT DOMAIN 102 111 FRAMEWORK 5.
 FT DISULFID 111 111 BY SIMILARITY.
 FT NON-TER 111 111
 SO SEQUENCE 111 AA: 11966 MW: 0C88B2F37CE24F CRC64:

Query Match 86.9%; Score 33; DB 1; Length 111;
 Best Local Similarity 87.4%; Pred. No. 1.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNORPS 7
 111111
 DB 51 EDNORPS 57

RESULT 6

LV6C_HUMAN STANDARD; PRT; 111 AA.
 AC P06317; 1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DE 15-JUL-1998 (Rel. 38, Last annotation update)
 DE IG LAMBDA CHAIN V-VI REGION SUP.
 OS Homo sapiens (human)
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_TaxID=9606;
 RN 1
 RP SEQUENCE.
 RA Solomon A., Kyle R.A., Frangione B.;
 RT "Light chain variable region subgroups of monoclonal immunoglobulins
 in amyloidosis AL.";
 RL (in) Glenner G.G., Osseman E.F., Benditt E.P., Calkins E.,
 RL Cohen A.S., Zucker-Franklin D. (eds.);
 DR PIR: M01988; F08454; P01719; P01719;
 DR HSP: P01703; 7FMSU.
 DR InterPro: IP003006;
 DR Pfam: PF00047; 19; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 22 FRAMEWORK 1.
 FT DOMAIN 2 36 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 50 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 57 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 5 58 91 FRAMEWORK 4.
 FT DOMAIN 6 92 100 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 7 101 111 FRAMEWORK 4.
 FT NON_TER 112 111 BY SIMILARITY.
 FT SEQUENCE 111 AA; 12247 MW; 0941D547D963598 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 111;
 Best Local Similarity 85.7%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EDNORPS 7
 111111
 DB 51 EDNORPS 57

RESULT 7
 YSL1_CAMEL STANDARD; PRT; 460 AA.
 AC Q09370;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE 2177 NUCLEOTIC ACID SEQUENCE FROM N.A.
 DE 2177 NUCLEOTIC ACID SEQUENCE FROM N.A.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditioidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 CC NCBI_TaxID=6239;
 RN 111
 RP SEQUENCE FROM N.A.
 RN STRAIN=BRISTOL N2;
 RC

RA Anderson K.;
 CC Submitted (JUL-1995) to the EMBL/GenBank/DBP databases.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use, and the data are made available as long as its content is in no way
 CC modified and this agreement is acknowledged by and for commercial
 CC entities requires a license agreement (see <http://www.elsb.ch/announce/>
 CC or send an email to license@elsb.ch)
 CC -----
 CC EMBL: U01321; AAC00044.1;
 DR Wormpep: U01321; CED089.
 KW Immunoglobulin protein.
 KW NCBI_TaxID=9606;
 DE 15-JUL-1998 (Rel. 38, Last sequence update)
 DE IG LAMBDA CHAIN V-VI REGION SUP.
 OS Homo sapiens (human)
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE.
 RA Solomon A., Kyle R.A., Frangione B.;
 RT "Light chain variable region subgroups of monoclonal immunoglobulins
 in amyloidosis AL.";
 RL (in) Glenner G.G., Osseman E.F., Benditt E.P., Calkins E.,
 RL Cohen A.S., Zucker-Franklin D. (eds.);
 DR PIR: M01988; F08454; P01719; P01719;
 DR HSP: P01703; 7FMSU.
 DR InterPro: IP003006;
 DR Pfam: PF00047; 19; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT NON_TER 108 108
 FT SEQUENCE 108 AA; 11342 MW; BBE8BD9C9C9E451 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 460;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNORPS 7
 111111
 DB 153 ODNORPA 159

RESULT 8
 LV5A_HUMAN STANDARD; PRT; 108 AA.
 AC P01719;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 38, Last annotation update)
 DE IG LAMBDA CHAIN V-VI REGION DEL.
 OS Homo sapiens (human)
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE.
 RA Solomon A., Kyle R.A., Frangione B.;
 RT "Light chain variable region subgroups of monoclonal immunoglobulins
 in amyloidosis AL.";
 RL (in) Glenner G.G., Osseman E.F., Benditt E.P., Calkins E.,
 RL Cohen A.S., Zucker-Franklin D. (eds.);
 DR PIR: M01988; F08454; P01719; P01719;
 DR HSP: P01703; 7FMSU.
 DR InterPro: IP003006;
 DR Pfam: PF00047; 19; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT NON_TER 108 108
 FT SEQUENCE 108 AA; 11342 MW; BBE8BD9C9C9E451 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 108;
 Best Local Similarity 71.4%; Pred. No. 6.7;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EDNORPS 7
 111111
 DB 48 EDNORPA 54

RESULT 9
 Y1E2_HSV4 STANDARD; PRT; 332 AA.
 AC Q12748;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 OS Herpesviridae; Herpesvirinae; Gammaherpesviridae; Gammaherpesvirinae;
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RN STRAIN=BRISTOL N2;
 RC

DE HYPOTHETICAL PROTEIN IN IE2 5' REGION (P3A0CHNT).
 OS Bovine herpesvirus type 4 (latency non-inducing, herpesviridae;
 OC Gammaherpesvirinae;
 NCBI_TaxID=10355;
 RN [1]
 CC SEQUENCE FROM N.A.
 RX MEDLINE-9124571; PubMed-830465;
 RA von Sarsen V.L.;
 RT A study of the evolution of a bovine herpesvirus 4 immediate-early RNA
 RL encoding a homolog of the Epstein-Barr virus R transactivator.
 CC J. Virol. 67:773-784(1993).
 CC -1- SIMILARITY: TO EBV BRF2.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L01039; AAA46056.1; -
 DR EMBL: L01039; AAA46056.1; -
 DR EMBL: L01039; AAA46056.1; -
 FT HYPOTHETICAL PROTEIN.
 FT NON_TER
 FT 1
 SO SEQUENCE 332 AA: 37951 MW; E0B6FAF287CC315 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 332;
 Best Local Similarity 81.3%; Pred. No. 24;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNOPR 6
 DB 11 EBNORP 16
 ID 1:|||||
 YLII ECOLI STANDARD: PRT; 371 AA.
 AC P75804;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HYPOTHETICAL 41.1 KDA PROTEIN IN MODA-DACC INTERGENIC REGION
 DE PRECURSOR.
 GN YLII.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Bacteriella.
 NCBI_TaxID=562;
 RN [1]
 CC SEQUENCE FROM N.A.
 RX STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blattner F.R.; Plunkett G., III; Bloch C.A.; Perna N.T.; Burland V.;
 RA Riley M.; Collado-Vides J.; Glasner J.D.; Rode C.K.; Mayhew G.E.;
 RA Gregory J.; Davis N.W.; Kirkpatrick H.A.; Goeden K.A.; Rose B.D.;
 RA White complete genome sequence of Escherichia coli K-12.
 CC Science 277:1453-1474(1997).
 CC [2]
 CC SEQUENCE FROM N.A.
 RX STRAIN-K12;
 RX MEDLINE-97061202; PubMed-8905232;
 RA Saito N.; Aiba H.; Baba T.; Fierke K.; Hayashi K.; Honjo A.;
 RA Ishida T.; Itoh T.; Kajihara M.; Kanai K.; Kashiuchi K.;
 RA Kimura S.; Kitagawa M.; Makino S.; Miki T.; Mizobuchi K.;
 RA Mochi H.; Motomura K.; Nakamura H.; Nishio Y.; Saito N.;
 RA Sempel G.; Seki Y.; Tagami H.; Takemoto K.; Wada C.; Yamamoto Y.;
 RA Yano M.; Horiiuchi T.;
 CC A 718-kb DNA sequence of the Escherichia coli K-12 genome

FT corresponding to the 12,7-28.0 min region on the linkage map.
 RL DNA Res. 3:137-155(1996).
 CC -1- SIMILARITY: STRONG; TO SYNCHOCYSTIS PCC 6803 SUR1508 AND SOME, TO
 CC A-CALDONETICUS GLUCOSE DEHYDROGENASE-B (GDH).
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: F0000186; AAC71923.1; -
 DR EMBL: F0000186; AAC71923.1; -
 DR EMBL: F0000186; AAC71923.1; -
 FT Hypothetical protein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 371
 FT HYPOTHETICAL PROTEIN YLII.
 FT NON_TER
 FT 1
 SO SEQUENCE 371 AA: 41054 MW; 920808FA302F5095 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 371;
 Best Local Similarity 71.4%; Pred. No. 27;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNOPRS 7
 DB 166 EBNORPT 172
 ID 1:|||||
 EYV4_HUMAN STANDARD: PRT; 551 AA.
 AC P43466;
 DT 04-DEC-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADENOVIRUS E1A ENHANCER BINDING PROTEIN (E1A-F) (ETS TRANSLLOCATION
 DE VARIANT 4) (FRAGMENT).
 GN EYV4 OR E1A-F.
 OS Homo sapiens (human).
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN [1]
 CC SEQUENCE FROM N.A.
 RX MEDLINE-95293380; PubMed-7774926;
 RA Friedman L.S.; Ostermeyer E.A.; Lynch E.D.; Szabo C.I.; Meza J.E.;
 RA Anderson L.A.; Dool F.; Lee M.K.; Kowall S.B.; Ellison J.;
 RA *2 genes from chromosome 17q21: cloning, sequencing, and
 RT characterization of mutations in breast cancer families and tumors.*;
 RL Genomics 25:256-263(1995).
 RN [2]
 CC SEQUENCE OF 90-551 FROM N.A.
 RX MEDLINE-93181246; PubMed-861656;
 RX STRAIN-K12 / MG1655;
 RA *Isolation of a cDNA encoding the adenovirus E1A enhancer binding
 RT protein: a new human member of the ets oncogene family.*;
 RL Nucleic Acids Res. 21:547-553(1993).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE ENHANCER OF
 CC THE ADENOVIRUS E1A GENE; THE CORE-BINDING SEQUENCE IS
 CC 5'-TACGACGACTGCG-3' (1).
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

or send an email to license@lsb-sib.ch.

CC EMBL: U08018; AA55591.1; -
 DR EMBL: U12765; BAA0234.1; -
 DR HSSP: P14921; 28TW. -
 DR TRANSFAC: T00685; -
 DR MIM: 600711; -
 DR InterPro: IPR000418; -
 DR PROSITE: PS00345; ETS_DOMAIN.1; -
 DR PROSITE: PS00346; ETS_DOMAIN.2; 1.
 DR PROSITE: PS00061; ETS_DOMAIN.3; 1.
 DR DNA-binding; Nuclear protein; Activator; Transcription regulation.
 KW DNA-binding; Nuclear protein; Activator; Transcription regulation.
 FT DOMAIN 1 116 142 ASP/GLU-RICH (ACIDIC).
 FT DNAS_BIND 408 488 GLN-RICH.
 FT DNAS_BIND 91 94 CNGS-DMSD (IN REF. 2).
 FT CONFLICT 91 94
 SEQUENCE 551 AA: 60570 MW: 90649GBAABDBDB CRC64;

Query Match 78.9% Score 30; DB 1; Length 551;
 Best Local Similarity 83.3% Pct: 42;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DNGRPS 7
 Db 501 DNGRPA 506

RESULT 12

ETV4_MOUSE STANDARD: PRT; 555 AA.

AC P28132; 01-OCT-1992 (Rel. 24, Created)
 DT 01-OCT-1992 (Rel. 24, Last sequence update)
 DE POLYOMAVIRUS ENHANCER ACTIVATOR 3 (PEA3 PROTEIN) (ETS TRANSLLOCATION
 DE VARIANT 4).
 GN ETV4 OR PEA3 OR PEA-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] TaxID=10050;
 RX MEDLINE=92192459; PubMed=1547944;
 RA Xin J.-H., Cowie A., Lachance P., Hassell J.A.;
 FT Ets oncogene family that is differentially expressed in mouse
 FT Genes Dev. 6:481-496(1992).
 RL
 CC - FUNCTION: BINDS TO THE PEA3 NOTIF (5'-AGCAAG-3'). MAY PLAY A
 CC REGULATORY ROLE DURING EMBRYOGENESIS.
 CC - SUBCELLULAR LOCATION: NUCLEUS.
 CC - TISSUE SPECIFICITY: EPIDIDYMIS AND THE BRAIN.
 CC - PRT: PHOSPHORYLATED.
 CC - SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC or send an email to license@lsb-sib.ch.
 CC EMBL: X63190; CAA44872.1; -
 DR PIR: S24061; S24061.
 DR HSSP: P14921; 28TW.
 DR TRANSFAC: T00684; -
 DR MIM: 600711; -
 DR InterPro: IPR000418; -

PIR: P00178; ETS.1
 DR PRINTS: PR00454; ETSDOMAIN.
 DR PROSITE: PS00345; ETS_DOMAIN.1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN.2; 1.
 DR PROSITE: PS00061; ETS_DOMAIN.3; 1.
 DR DNA-binding; Nuclear protein; Activator; Transcription regulation.
 KW DNA-binding; Nuclear protein; Activator; Transcription regulation.
 FT DOMAIN 1 116 142 ASP/GLU-RICH (ACIDIC).
 FT DNAS_BIND 408 488 GLN-RICH.
 FT DNAS_BIND 91 94 CNGS-DMSD (IN REF. 2).
 FT CONFLICT 91 94
 SEQUENCE 555 AA: 60846 MW: 27807GBAABDBDB CRC64;

Query Match 78.9% Score 30; DB 1; Length 555;
 Best Local Similarity 83.3% Pct: 42;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DNGRPS 7
 Db 505 DNGRPA 510

RESULT 13

ITR_HUMAN STANDARD: PRT; 620 AA.

AC Q08881; 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DE TYROSINE-PROTEIN KINASE ITR/TSK (EC 2.7.10.12) (T-CELL-SPECIFIC
 DE KINASE) (TYROSINE-PROTEIN KINASE LYX) (KINASE EMT).
 GN ITR OR LYX OR EMT.
 OS Homo sapiens (human).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1] NCBI_TaxID=9606;
 RX MEDLINE=93279365; PubMed=8504851;
 RA Tanaka N., Aaso H., Ohnishi K., Nakamura M., Suganuma K.;
 FT A novel human tyrosine kinase gene inducible in T cells by
 FT PMA. J. Biol. Chem. 269:12411-12415(1994).
 RL FEBS Lett. 344:115-119(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=9337354; PubMed=8364206;
 RA Gibson S., Leung B., Squire J.A., Hill M., Arima N., Goss P.,
 FT Identification of a novel human T-cell-specific tyrosine kinase
 FT and characterization of a novel human T-cell-specific tyrosine kinase
 FT on chromosome 5q. J. Biol. Chem. 269:12411-12415(1994).
 RL Blood 82:1561-1572(1993).
 CC - FUNCTION: PLAYS A ROLE IN T CELL PROLIFERATION AND
 CC DIFFERENTIATION.
 CC - SUBCELLULAR LOCATION: LOCALIZES TO CELL SURFACE RECEPTORS IN THE
 CC PLASMA MEMBRANE OF T-CELLS (BY SIMILARITY).
 CC CD28, CD2) IN T-CELLS (BY SIMILARITY).
 CC - TISSUE SPECIFICITY: T-CELL LINES AND NATURAL KILLER CELL LINES.
 CC - INDUCTION: BY INTERLEUKIN 2.
 CC - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC - SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC DOMAIN. BELONGS TO THE SH2-CONTAINING TYROSINE KINASES IN THE CATALYTIC
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC or send an email to license@lsb-sib.ch.

```

CC -----
DR EMBL: D13720; AAA02873.1; -
DR EMBL: L01717; BA036748.1; -
DR EMBL: AF015166; AA020722.2; -
DR EMBL: S33456; S33253; -
DR HSP: Q03556; 1AM7; -
DR MIM: 186973; -
DR InterPro: IPR000719; -
DR InterPro: IPR000980; -
DR InterPro: IPR001453; -
DR InterPro: IPR001563; -
DR InterPro: IPR001849; -
DR Pfam: PF00779; BTK.1; -
DR Pfam: PF00169; PK.1; -
DR Pfam: PF00017; SH2.1; -
DR Pfam: PF00048; SH3.1; -
DR Pfam: PF00008; SH3 domain; 1; -
DR PRINTS: PR00109; SH2KINASE; -
DR PRINTS: PR00401; SH3DOMAIN; -
DR PRINTS: PR00402; TCBTKDOMAIN; -
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1; -
DR PROSITE: PS00111; PROTEIN_KINASE_TYR.1; -
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1; -
DR PROSITE: PS00002; SH3.1; -
DR PROSITE: PS00003; PH_DOMAIN.1; -
DR Transferrase: Tyrosine-protein kinase: Phosphorylation;
KW ATP-binding; SH2 domain; SH3 domain;
FT DOMAIN 1 4 111 PH;
FT DOMAIN 171 231 SH2;
FT DOMAIN 271 338 SH3;
FT NR_BIND 363 615 ATP (BY SIMILARITY);
FT BINDING 391 391 ATP (BY SIMILARITY);
FT ACT_SITE 482 482 BY SIMILARITY;
FT MOD_RES 512 512 PHOSPHORYLATION (ATTO-) (BY SIMILARITY);
FT CONFIDAT 531 531 92.607;
SQ SEQUENCE 620 AA; 71831 MW; DA6396BD209319D CRC64;
OY 1 EDNORP 6
Query Match 78.98; Score 30; DB 1; Length 620;
Best Local Similarity 83.38; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 162 EDNRRP 167

```

```

RL Int. J. Pept. Protein Res. 29:21-39(1987).
RC TISSUE=Thymus;
RC MEDLINE=85298222; PubMed=2994041;
RA Williams K.R., Stone K.L., Lopreati M.B., Merrill B.M., Planch S.R.;
RT Amino acid sequence of the UPI and the thymus stabilizing
RT protein and its homology to an analogous protein from mouse
RT proc. Natl. Acad. Sci. U.S.A. 82:5666-5670(1985).
RN (3)
RP SEQUENCE OF 1-184.
RC TISSUE=Thymus; PubMed=3941105;
RX MEDLINE=86083929; PubMed=3941105;
RA High pressure liquid chromatography purification of UPI and up2, two
RT related single-stranded nucleic acid-binding proteins from calf
RT thymus;
RL J. Biol. Chem. 261:878-883(1986).
CC -1- FUNCTION: INVOLVED IN THE PACKAGING OF PRE-mRNA INTO hnRNP
CC PARTICLES; TRANSPORT OF PRE-mRNA FROM THE NUCLEUS TO THE
CC CYTOPLASM; AND MODULATE SPLICING SITE SELECTION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR. SHUTTLES CONTINUOUSLY BETWEEN THE
CC NUCLEUS AND THE CYTOPLASM ALONG WITH MRNA. COMPONENT OF
CC RIBONUCLEOSOMES.
CC -1- PFM: UPI IS DERIVED FROM A1 BY PROTEOLYTIC DEGRADATION.
CC -1- SIMILARITY: BELONGS TO THE A/B GROUP OF hnRNP, WHICH ARE BASIC AND
CC -1- GUT-RICH PROTEINS.
CC -1- SUBCELLULAR LOCATION: 2 RNA RECOGNITION MOTIFS (RRM).
CC DR PIR: A272A1; A272A1.
CC DR HSP: A26526; A26526.
CC DR InterPro: IPR00504; -
CC DR PROSITE: PS00076; ARM.2; -
CC DR PROSITE: PS00102; RRM.2; -
CC DR Nucleic acid-binding protein: RNA-binding; Repeat: Ribonucleoprotein;
KW Methylation.
FT DOMAIN 3 93 GLOBULAR A DOMAIN;
FT DOMAIN 94 184 RNA-BINDING (RRM) 1;
FT DOMAIN 104 183 RNA-BINDING (RRM) 2;
FT MOD_RES 193 193 BLOCKED;
FT NON_TER 195 195 METHYLATION (DI-);
SQ SEQUENCE 195 AA; 22132 MW; 448090F547067ED1 CRC64;
OY 1 EDNORP 6
Query Match 76.38; Score 29; DB 1; Length 195;
Best Local Similarity 83.38; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 92 EDORP 97

```

```

RESULT 14
DB 162 EDNRRP 167
RC TISSUE=Thymus;
RC MEDLINE=87193538; PubMed=3032834;
RA Merrill B.M., Lopreati M.B., Stone K.L., Williams K.R.;
RT Amino acid sequence of UPI, an hnRNP-derived single-stranded nucleic
RT acid binding protein from calf thymus;

```

```

RESULT 15
DB 92 EDORP 97
RC TISSUE=Thymus;
RC MEDLINE=86083929; PubMed=3941105;
RA High pressure liquid chromatography purification of UPI and up2, two
RT related single-stranded nucleic acid-binding proteins from calf
RT thymus;
RL J. Biol. Chem. 261:878-883(1986).
CC -1- FUNCTION: INVOLVED IN THE PACKAGING OF PRE-mRNA INTO hnRNP
CC PARTICLES; TRANSPORT OF PRE-mRNA FROM THE NUCLEUS TO THE
CC CYTOPLASM; AND MODULATE SPLICING SITE SELECTION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR. SHUTTLES CONTINUOUSLY BETWEEN THE
CC NUCLEUS AND THE CYTOPLASM ALONG WITH MRNA. COMPONENT OF
CC RIBONUCLEOSOMES.
CC -1- PFM: UPI IS DERIVED FROM A1 BY PROTEOLYTIC DEGRADATION.
CC -1- SIMILARITY: BELONGS TO THE A/B GROUP OF hnRNP, WHICH ARE BASIC AND
CC -1- GUT-RICH PROTEINS.
CC -1- SUBCELLULAR LOCATION: 2 RNA RECOGNITION MOTIFS (RRM).
CC DR PIR: A272A1; A272A1.
CC DR HSP: A26526; A26526.
CC DR InterPro: IPR00504; -
CC DR PROSITE: PS00076; ARM.2; -
CC DR PROSITE: PS00102; RRM.2; -
CC DR Nucleic acid-binding protein: RNA-binding; Repeat: Ribonucleoprotein;
KW Methylation.
FT DOMAIN 3 93 GLOBULAR A DOMAIN;
FT DOMAIN 94 184 RNA-BINDING (RRM) 1;
FT DOMAIN 104 183 RNA-BINDING (RRM) 2;
FT MOD_RES 193 193 BLOCKED;
FT NON_TER 195 195 METHYLATION (DI-);
SQ SEQUENCE 195 AA; 22132 MW; 448090F547067ED1 CRC64;
OY 1 EDNORP 6
Query Match 76.38; Score 29; DB 1; Length 195;
Best Local Similarity 83.38; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 92 EDORP 97

```

RA Peck O., Tordo N., Keth G.;
 RT Sequence of the 3863' nucleotides of the genome of the AVO1 strain
 RT in transcriptome.
 RT in transcriptome.
 RT Biochimie 70:1019-1029(1988).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL, outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use and profile institutions as long as its content is in no way
 CC modified and the EMBL is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: X13357; CAA31736.1; .
 CC EIR: S07816; MFVNAV.
 CC PROBABLY: P00000; MatriX protein; Envelope protein.
 CC SEQUENCE 502 AA; 23231 MW; DD139AE8BCF92D2 CRC64;

Query Match 76.3%; Score 29; DB 1; Length 202;
 Best Local Similarity 71.4%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 EDOKPS 7
 11 1:11
 DB 14 EDOKPS 20

Search completed: November 19, 2001, 08:25:36
 Job time: 724 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

NOVEMBER 19, 2001, 08:25:03 ; Search time 81.19 Seconds
(without alignments)
11.407 Million cell updates/sec

Title: US-09-610-118-65
Perfect score: 38

Scoring table: BLOSUM62

Searched: 425026 seqs, 132305027 residues

total number of hits satisfying chosen parameters:

Maximum DB seq length: 2000000000

Post-processing: Minimum match 0%

Listing first 45 summaries

Database : SPTREMBL_16:*

Listing first 45 summaries

```

1:  sp.archaea:.*
2:  sp.bacteria:.*
3:  sp.fungi:.*
4:  sp.human:.*
5:  sp.invertebrate:.*
6:  sp.mammal:.*
7:  sp.mbc:.*
8:  sp.organelle:.*
9:  sp.phage:.*
10: sp.plant:.*
11: sp.rodent:.*
12: sp.unclassified:.*
13: sp.vertebrate:.*
14: sp.virus:.*

```

PRED. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	85.5	265	2	049649	049649 mycobacteri
2	34	85.5	265	2	049649	049649 mycobacteri
3	33	86.8	476	5	080856	080856 arabisolus
4	33	86.8	476	5	080856	080856 arabisolus
5	33	86.8	491	13	099201	049555 Leishmania
6	33	86.8	491	13	057586	049555 Leishmania
7	32	84.2	411	5	009534	009534 Bradyrhizob
8	31	81.6	161	2	09P1K9	09P1K9 Bradyrhizob
9	31	81.6	161	2	09P1K9	09P1K9 Bradyrhizob
10	30	78.9	738	5	09VAC9	09VAC9 diosporilla
11	30	78.9	85	2	09L587	09L587 chlamydia t
12	30	78.9	232	10	022922	022922 arabisolus t
13	30	78.9	331	2	09P1K6	09P1K6 Bradyrhizob
14	30	78.9	331	2	09P1K6	09P1K6 Bradyrhizob
15	30	78.9	355	2	09P1K6	09P1K6 Bradyrhizob
16	30	78.9	361	14	09VAC9	09VAC9 diosporilla
17	30	78.9	361	14	09VAC9	09VAC9 diosporilla
18	30	78.9	390	9	09P1K6	09P1K6 Bradyrhizob
19	30	78.9	409	10	09S6C6	09S6C6 mycoplasma
20	30	78.9	430	10	09S6C6	09S6C6 mycoplasma
21	30	78.9	522	2	085210	085210 virbio chlo

20	30	78.9	5.22	2	0.9K39.4	
21	30	78.9	6.64	10	0.6A58.9	arabidopsis
22	30	78.9	8.82	11	0.9L16.5	mus musculus
23	30	78.9	8.92	11	0.9L16.5	mus musculus
24	30	78.9	24.73	11	0.9O28.4	rat
25	29	76.3	7.6	14	0.8B28.3	snakelhead r
26	29	76.3	7.6	14	0.8B28.3	snakelhead r
27	29	76.3	1.12	14	0.9Z09.0	human
28	29	76.3	1.12	14	0.9Z09.0	human
29	29	76.3	1.42	6	0.1K35.5	hom sapien
30	29	76.3	1.79	4	0.1K39.6	undifferent
31	29	76.3	1.79	4	0.1K39.6	undifferent
32	29	76.3	1.79	4	0.1K39.6	undifferent
33	29	76.3	1.79	4	0.1K39.6	undifferent
34	29	76.3	2.02	14	0.9J13.7	hom sapien
35	29	76.3	2.36	12	0.9Y16.7	galius galli
36	29	76.3	3.12	1	0.9M00.4	halobacter
37	29	76.3	3.12	1	0.9M00.4	halobacter
38	29	76.3	3.17	4	0.9S02.4	hom sapien
39	29	76.3	3.28	10	0.9Z1X.7	arabidopsis
40	29	76.3	3.76	6	0.9Y5V.3	sus scrofa
41	29	76.3	4.00	10	0.9S05.7	brassica ju
42	29	76.3	4.73	11	0.9Z2M.0	thermoga
43	29	76.3	4.77	13	0.9S32.2	xenopus lae
44	29	76.3	4.77	13	0.9S32.2	xenopus lae
45	29	76.3	4.77	13	0.9S32.2	xenopus lae
46	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
47	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
48	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
49	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
50	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
51	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
52	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
53	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
54	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
55	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
56	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
57	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
58	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
59	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
60	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
61	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
62	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
63	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
64	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
65	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
66	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
67	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
68	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
69	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
70	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
71	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
72	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
73	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
74	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
75	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
76	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
77	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
78	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
79	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
80	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
81	29	76.3	5.10	11	0.9Y5H.6	xenopus lae
82	29	76.3	5.10	1		

ALIGNMENTS

	RESULT	1		PRT.	266 AA.
ID	049840		PRELIMINARY:		
AD	049849				
DT	01-NOV-1996	(TREMBLREL_01)	Created		
DT	01-NOV-1996	(TREMBLREL_01)	Last sequence update		
DT	01-NOV-1996	(TREMBLREL_01)	Last annotation update		
DE	B2325_F2.77.				
OS	Mycobacterium leprae.				
OX	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;				
NC	NHJ_TaxID=1769;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RL	Robison K.;				
RA	Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.				
RD	[2]				
RP	SEQUENCE FROM N.A.				
RL	Smith D.R.;				
RA	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.				
RD	[3]				
RP	SEQUENCE FROM N.A.				
RL	Robison K.;				
RA	Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.				
RD	EMBL accession number F17281.1				
SQ	Sequence 266 AA; 29602 MW; 02C50A1B4E36EC82 CIRC4;				
	Query Match				
	Best Local Similarity	89.5%; Score 34; DB 2; Length 266;			
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	1 EDMPOR 6				
DB	103 EDMOPR 108				
RESULT	2				
ID	080896		PRELIMINARY:		
AD	080896				
AC	080896;		PRT.	704 AA.	
	01-NOV-1998 (TREMBLREL_08, Created)				

01-NOV-1998 (TREMBLrel_08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel_08, Last annotation update)
 DE PUTATIVE CONDENSIN PROTEIN.
 GN T26B15.15.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsia.
 RN [1]_TaxID=7902;
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV. COLUMBIA;
 RA Ronsaley S.D., Keul S., Ilin X., Ketchum K.A., Crosby M.L.,
 RA Brandt R.C., Sykes S.M., Mason T.M., Karlavagge A.R., Adams M.D.,
 RA Somerville C.R., Lander J.C.,
 RA The Arabidopsis Genome Initiative
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004681; AAC2941.1; -
 SO SEQUENCE 704 AA; 79017 MW; 69C8B8FD6C040FA CRC64;

Query Match 89.8%; Score 34; DB 10; Length 704;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DNGRPS 7
 DB 330 DNGRPS 336
 |||||||

RESULT 3
 043955 PRELIMINARY; PRT; 478 AA.
 AC 043955
 DT 01-JUN-1998 (TREMBLrel_06, Created)
 DT 01-JUN-1998 (TREMBLrel_06, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel_08, Last annotation update)
 DE NUPN1.
 GN TOR.
 OS Leishmania mexicana.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 NCBI_TaxID=5665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=LEV 28;
 RA MEDLINE=98135664; PubMed=9476797;
 RX MEDLINE=98135664; PubMed=9476797;
 RX STRAIN=LEV 28;
 RL Local. Blochman, Parastolli, 90:505-511(1997).
 RL EMBL: AF016373; AAC3923.1; -
 SO SEQUENCE 478 AA; 52273 MW; 6036DDE0210CA1 CRC64;

Query Match 86.8%; Score 33; DB 5; Length 478;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DNGRPS 7
 DB 342 DNGRPS 347
 |||||||

RESULT 4
 09P001 PRELIMINARY; PRT; 491 AA.
 AC 09P001
 DT 01-MAY-2000 (TREMBLrel_13, Created)
 DT 01-MAY-2000 (TREMBLrel_13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel_16, Last annotation update)
 DE PEA3.
 GN Brachydanio rerio (zebrafish).
 SO Brachydanio rerio (zebrafish) (zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Osteichthys;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20005800; PubMed=10534622;
 RX MEDLINE=20005800; PubMed=10534622;
 RX STRAIN=Steindler H.;
 RL "Expression of the Ets transcription factors erm and pea3 in early
 zebrafish development.";
 RT Mech. Dev. 88:233-236(1999).
 DR HSP; P14921; 287T.
 DR EMBL: AF168008; AAD50434.1; -
 DR InterPro: IPR002413; -
 DR Pfam: PF00178; Ets_1.
 DR PRINTS: PR00454; ETSDOMAIN.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR SMART: SM00413; ETS; 1.
 SO SEQUENCE 491 AA; 55676 MW; 11AB8A813BAE7B CRC64;

Query Match 86.8%; Score 33; DB 13; Length 491;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DNGRPS 7
 DB 440 DNGRPS 445
 |||||||

RESULT 5
 057586 PRELIMINARY; PRT; 494 AA.
 AC 057586
 DT 01-JUN-1998 (TREMBLrel_06, Created)
 DT 01-JUN-1998 (TREMBLrel_06, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel_16, Last annotation update)
 DE ETS-DOMAIN TRANSCRIPTION FACTOR PEA3.
 GN PEA3.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Osteichthys;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BROWN L.A., YAMASAKI A.D., SCHILLING T.F., JONETT T., BAERT J.L.,
 RA BROWN L.A., YAMASAKI A.D., SCHILLING T.F., JONETT T., BAERT J.L.,
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AJ003200; CAA05980.1; -
 DR HSP; P14921; 287T.
 DR ZFIN: ZDB-GENE-990415-71; PEA3.
 DR InterPro: IPR000419; -
 DR InterPro: IPR002413; -
 DR PRINTS: PR00454; ETSDOMAIN.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS50061; ETS_DOMAIN_3; 1.
 DR SMART: SM00413; ETS; 1.
 SO SEQUENCE 494 AA; 55620 MW; 81495533DA25C362 CRC64;

Query Match 86.8%; Score 33; DB 13; Length 494;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DNGRPS 7
 DB 443 DNGRPS 448
 |||||||

[illegible]

InterPro: IP000822; 7
 RC STRAIN-PROTEIN: C21H2
 DR SMART: SMO0355; ZINC_C2H2; 1
 KW DVA-binding; Metal-binding; zinc-finger.
 SQ SEQUENCE 738 AA: 79951 MW: 5F6E3C3AC41795C CRC64:

Query Match 81.6%; Score 31; DB 5; Length 738;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 2; Mismatches 0; Gaps 0;

OY 1 EDNRPS 7
 DB 730 QENDRPS 736

RESULT 9
 ID 091987 PRELIMINARY; PRT: 85 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 16, Last annotation update)
 DE MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
 GN CMPL.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 NC NCBI_TaxID=813;
 RN 11 SEQUENCE FROM N.A.
 RC STRAIN-CA589;
 RA MEDLINE=20085123; PubMed=10618077;
 RA Shlor I., N'Doye I., Brumblay H., Diop K., Gueye-Mdiaye A., Sankala J.L.,
 M'Foliar K., N'Doye I., Hsieh C.C., Mboup S., Kanki P.J.;
 RT Molecular epidemiology of genital Chlamydia trachomatis infection in
 high-risk women in Senegal (abstract 18138-145(2000)).
 DR EMBL: AF178257; AAF26695.1; JOINED.
 DR EMBL: AF178258; AAF26695.1; JOINED.
 DR EMBL: AF178259; AAF26695.1; JOINED.
 DR InterPro: IP000604; 1
 FT NON_TER 85 85
 FT SEQUENCE 85 AA: 8551 MW: A183857B82CB076B CRC64:

Query Match 78.9%; Score 30; DB 2; Length 85;
 Best Local Similarity 71.4%; Pred. No. 18;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDNRPS 7
 DB 20 EDNRPS 26

RESULT 10
 ID 022922 PRELIMINARY; PRT: 232 AA.

DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE 515000000K PROTEIN 028 180000.
 GN T09D09.7
 OS Arabidopsis thaliana (House-ear cross).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxID=3702;
 RN 11
 FT

RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLDWATER;
 RA Rounsley S.O., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
 RA Sykes S.M., Mason T.M., Kettlewell A.R., Adams M.D., Somerville G.R.,
 RA Venter J.C.;
 RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF000306; AAL0931.1;
 DR EMBL: AF000307; AAL0932.1;
 DR Model: 26539; Arth:1206;26539.
 DR InterPro: IP000504; 1
 DR InterPro: IP000834; 1
 DR Pfam: PF00076; 1
 DR PROSITE: PS00133; CARBOXYPEPT_2K.2; UNKNONM.1.
 DR SMART: SMO0350; RNF; A006607B1084E99 CRC64:
 SQ SEQUENCE 232 AA: 46237 MW: A006607B1084E99 CRC64:

Query Match 78.9%; Score 30; DB 10; Length 232;
 Best Local Similarity 71.4%; Pred. No. 37;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNRPS 7
 DB 119 EDNRPS 125

RESULT 11
 ID 09876 PRELIMINARY; PRT: 273 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ORF_ID=020947 (FRAGMENT).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NC NCBI_TaxID=562;
 RN 11
 RC STRAIN-K12; PubMed=890523;
 RA MEDLINE=7061202; PubMed=890523;
 RA Ikemoto K., Inada T., Itoh T., Kajiya M., Kanai K., Kashiwano K.,
 RA Ikemoto K., Inada T., Itoh T., Kajiya M., Kanai K., Kashiwano K.,
 RA Kimura S., Kikawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horikuchi T.
 FT A 845-859 Sequence of Escherichia coli K-12 Genome Corresponding
 FT to the 12,798 Region on the Linkage Map.
 RL DNA Res 3.137-151(1996).
 DR EMBL: D90721; BAB35532.1; 1
 FT NON_TER 273 273
 FT SEQUENCE 273 AA: 30059 MW: E27C16D648123C6D CRC64:

Query Match 78.9%; Score 30; DB 2; Length 273;
 Best Local Similarity 71.4%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDNRPS 7
 DB 166 EDNRPS 172

RESULT 12
 ID 09YH5 PRELIMINARY; PRT: 336 AA.

DT 01-MAY-1998 (TREMBLrel. 10, Created)
 DT 01-MAY-1998 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ETS DOMAIN PROTEIN (FRAGMENT).
 NC NCBI_TaxID=3702;
 RN 11
 FT

CN PRA1
 OC Gallus gallus (Chicken)
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 OC Actinopterygii: Aves: Neognathae, Galliformes, Phasianidae, Phasianinae:
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lilo J.H.: Gallo I., Anderson D.J., Lance-Jones C., Jansell T.M.,
 RT "Functionally related motor neuron pool and muscle sensory afferent
 RT Cell 95:393-407(1986).
 RL EMBL: AF075708; AAC97203.1; -;
 DR InterPro: IPR00048; -;
 DR InterPro: IPR002341; -;
 DR Pfam: PF00178; Ets; 1;
 DR PRINTS: PR00345; ETS_DOMAIN.1;
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1;
 DR SMART: SM00413; ETS_DOMAIN_3; 1;
 FT NON_TER 1 ETS; 1;
 FT SEQUENCE 336 AA; 3858 MW; 0507A0A11995FA8B CRC64;
 Query Match 78.9%; Score 30; DB 13; Length 336;
 Best Local Similarity 83.3%; Pred. No. 53;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 EDNGRPS 7
 Db 287 EDNGRPS 292
 RESULT 13
 ID 09F3F6 PRELIMINARY; PRT; 355 AA.
 AC 09F3F6;
 DT 01-MAR-2001 (TRENBERG, 16, Created)
 DT 01-MAR-2001 (TRENBERG, 16, Last sequence update)
 DE PURIFICATION SECRETED PROTEIN.
 GN ZSC04.18
 OS Streptomyces coelicolor.
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
 OC Actinomycetales: Streptomycetales: Streptomycetaceae: Streptomyces.
 NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seeger K.J., Harris D.;
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-A3(2); Parthill J., Barrett R.G., Rajandream M.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor ATCC 27061 chromosome."
 RL EMBL: AL392175; CAC08363.1; -;
 SO SEQUENCE 355 AA; 37716 MW; 3ED06B00F462BB8E CRC64;

Query Match 78.9%; Score 30; DB 2; Length 355;
 Best Local Similarity 71.4%; Pred. No. 56;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EDNGRPS 7
 Db 31 EDNGRPS 37

RESULT 14
 ID 09YMR9 PRELIMINARY; PRT; 361 AA.
 AC 09YMR9;
 DT 01-MAY-1999 (TRENBERG, 10, Created)
 DT 01-MAY-1999 (TRENBERG, 10, Last sequence update)
 DE LONR-55 PEPTIDE.
 OS Lymnaea dispar multiplexid nuclear polydrosis virus (LdNPV).
 OC Viruses: dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolydnavirus.
 NCBI_TaxID=10449;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:99124785; PubMed-9887315;
 RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
 RA Slavicek J.M., Rohmann G.F.;
 RT "Sequence and analysis of the genome of a baculovirus pathogenic for
 RT Lymnaea dispar."
 RL Virology 253:17-34(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
 RA Slavicek J., Rohmann G.F.;
 RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF081810; AAC70240.1; -;
 SO SEQUENCE 361 AA; 39655 MW; 76D2D1627EB9E402 CRC64;

Query Match 78.9%; Score 30; DB 14; Length 361;
 Best Local Similarity 71.4%; Pred. No. 57;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EDNGRPS 7
 Db 318 EDNGRPS 324

RESULT 15
 ID 09GRG0 PRELIMINARY; PRT; 366 AA.
 AC 09GRG0;
 DT 01-MAY-2000 (TRENBERG, 13, Created)
 DT 01-MAY-2000 (TRENBERG, 13, Last sequence update)
 DE LCB9A.
 GN LCB9A.
 OS Neisseria meningitidis.
 OC Bacteria: Proteobacteria: beta subdivision; Neisseriaceae: Neisseria.
 NCBI_TaxID=187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brewer N.E., Coulthart M.B., Tyler S.D.;
 RT "Analysis of the region encoding the putative capsular biosynthetic
 RT genes of the Neisseria meningitidis serogroup L."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF071145; AF071146; AF071147; -;
 SO SEQUENCE 366 AA; 42281 MW; F7A95F3843D1B67E CRC64;

Query Match 78.98; Score 30; DB 2; Length 366;
 Seed Local 58.38; Seed No. 58;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDNQR 6
 |||||
 DB 330 EDNQR 335

Search completed: November 19, 2001, 08:25:04
 Job time: 742 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

om protein - protein search, using sw model

Run on: November 19, 2001, 08:14:23 ; Search time 48.99 Seconds

12.439 Million cell updates/sec

US-09-610-118-66
Perfect score, 38
File:

Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62

Gapop 10.0 ,

Searched: 219241 seqs, 76174552 r

Total number of hits satisfying chosen parameters: 219241

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PTR 68.*

```
l: plr1:*
```

3: *
plt3:

4: pir4: *

Pred. No. is the number of results predicted.

and is derived by analysis of the tot

SUMMARY

Query	Result
1	1
2	1
3	1
4	1
5	1
6	1
7	1
8	1
9	1
10	1
11	1
12	1
13	1
14	1
15	1
16	1
17	1
18	1
19	1
20	1
21	1
22	1
23	1
24	1
25	1
26	1
27	1
28	1
29	1
30	1
31	1
32	1
33	1
34	1
35	1
36	1
37	1
38	1
39	1
40	1
41	1
42	1
43	1
44	1
45	1
46	1
47	1
48	1
49	1
50	1
51	1
52	1
53	1
54	1
55	1
56	1
57	1
58	1
59	1
60	1
61	1
62	1
63	1
64	1
65	1
66	1
67	1
68	1
69	1
70	1
71	1
72	1
73	1
74	1
75	1
76	1
77	1
78	1
79	1
80	1
81	1
82	1
83	1
84	1
85	1
86	1
87	1
88	1
89	1
90	1
91	1
92	1
93	1
94	1
95	1
96	1
97	1
98	1
99	1
100	1

NO.	CODE	NAME	BR	ID
1	0000	0000	0000	0000
2	0000	0000	0000	0000
3	0000	0000	0000	0000
4	0000	0000	0000	0000
5	0000	0000	0000	0000
6	0000	0000	0000	0000
7	0000	0000	0000	0000
8	0000	0000	0000	0000
9	0000	0000	0000	0000
10	0000	0000	0000	0000
11	0000	0000	0000	0000
12	0000	0000	0000	0000
13	0000	0000	0000	0000
14	0000	0000	0000	0000
15	0000	0000	0000	0000
16	0000	0000	0000	0000
17	0000	0000	0000	0000
18	0000	0000	0000	0000
19	0000	0000	0000	0000
20	0000	0000	0000	0000
21	0000	0000	0000	0000
22	0000	0000	0000	0000
23	0000	0000	0000	0000
24	0000	0000	0000	0000
25	0000	0000	0000	0000
26	0000	0000	0000	0000
27	0000	0000	0000	0000
28	0000	0000	0000	0000
29	0000	0000	0000	0000
30	0000	0000	0000	0000
31	0000	0000	0000	0000
32	0000	0000	0000	0000
33	0000	0000	0000	0000
34	0000	0000	0000	0000
35	0000	0000	0000	0000
36	0000	0000	0000	0000
37	0000	0000	0000	0000
38	0000	0000	0000	0000
39	0000	0000	0000	0000
40	0000	0000	0000	0000
41	0000	0000	0000	0000
42	0000	0000	0000	0000
43	0000	0000	0000	0000
44	0000	0000	0000	0000
45	0000	0000	0000	0000
46	0000	0000	0000	0000
47	0000	0000	0000	0000
48	0000	0000	0000	0000
49	0000	0000	0000	0000
50	0000	0000	0000	0000
51	0000	0000	0000	0000
52	0000	0000	0000	0000
53	0000	0000	0000	0000
54	0000	0000	0000	0000
55	0000	0000	0000	0000
56	0000	0000	0000	0000
57	0000	0000	0000	0000
58	0000	0000	0000	0000
59	0000	0000	0000	0000
60	0000	0000	0000	0000
61	0000	0000	0000	0000
62	0000	0000	0000	0000
63	0000	0000	0000	0000
64	0000	0000	0000	0000
65	0000	0000	0000	0000
66	0000	0000	0000	0000
67	0000	0000	0000	0000
68	0000	0000	0000	0000
69	0000	0000	0000	0000
70	0000	0000	0000	0000
71	0000	0000	0000	0000
72	0000	0000	0000	0000
73	0000	0000	0000	0000
74	0000	0000	0000	0000
75	0000	0000	0000	0000
76	0000	0000	0000	0000
77	0000	0000	0000	0000
78	0000	0000	0000	0000
79	0000	0000	0000	0000
80	0000	0000	0000	0000
81	0000	0000	0000	0000
82	0000	0000	0000	0000
83	0000	0000	0000	0000
84	0000	0000	0000	0000
85	0000	0000	0000	0000
86	0000	0000	0000	0000
87	0000	00		

T08080
680 2
84.6
33 33
T 2

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	84.6	650	2	T08080	probable myosinVa
2	33	84.6	650	2	E39559	hypothetical protein
3	33	84.6	534	2	A60163	Probable formate dehydrogenase
4	33	84.6	1037	2	A60163	Probable formate dehydrogenase
5	33	84.6	1945	2	T13937	Probable alpha-2(Ig) lambda chain V-gene
6	32	82.1	112	1	L6H44	Probable alpha-2(Ig) lambda chain V-gene
7	32	82.1	459	2	B37837	Pept protein - Staphylococcus aureus
8	32	82.1	571	2	E58356	hypothetical protein
9	32	82.1	571	2	E58356	hypothetical protein
10	31	79.5	1200	2	A10162	large receptor alpha-2(Ig) lambda chain V-gene
11	31	79.5	245	2	G84781	hypothetical protein
12	31	79.5	249	2	G84781	hypothetical protein
13	31	79.5	261	2	T15520	insulin-like growth factor receptor
14	31	79.5	271	2	J54584	hypothetical protein
15	31	79.5	271	2	T15113	hypothetical protein
16	31	79.5	374	2	A10195	hypothetical protein
17	31	79.5	430	2	A10195	hypothetical protein
18	31	79.5	783	2	B84423	probable isomylase
19	31	79.5	876	2	B96693	hypothetical protein
20	31	79.5	963	2	E51517	chitin synthase (F) replication protein
21	30	76.9	229	2	S94954	hypothetical protein
22	30	76.9	233	2	T73306	hypothetical protein
23	30	76.9	238	2	T15063	hypothetical protein
24	30	76.9	328	2	S63350	hypothetical protein
25	30	76.9	429	2	T16041	hypothetical protein
26	30	76.9	458	2	B96560	hypothetical protein
27	30	76.9	462	2	T52115	hypothetical protein
28	30	76.9	462	2	V6097	phosphatase-binding protein
29	30	76.9	624	2	T10377	p87 capsid protein

<hr/>					
RESULTS					
1					
708080					
Probable myrosinase-binding protein - rape					
N:Alternate names: jasmonate inducible protein					
C:Species:	Brassica napus (rape)				
C:Accession:	U00890	Sequence revision 21-May-1999	textL change 11-May-2000		
R:Gene(s), N.: Brandt, A.					
Planta 204,	295-304,	1998			
A>Title:	Two jasmonate-inducible myrosinase-binding proteins from Brassica napus L.				
A:Reference number:	216340.	MUID:98192006			
A:Accession:	T08080				
A:Status:	preliminary; translated from GR/EMBL/DDB3				
A:Accession:	U00890				
A:Length:	317	aa (mks)			
A:Cross-references:	PML:Y11483; NID-g1023101; PION:CAN72271.1;				
A:Experimental source:	cvt. global; isolate s4; young seedlings				
A>Note:	jasmonate inducible				
<hr/>					
Query Match		84.6%	Score 33;	DB 2;	
Best Local Similarity		71.4%	Pred. No. 38;		
Matches	5/	Conservative	2;	Mismatches	0;
Ox	2 YDSSNV B				
	:				
Db	308 YDSSNII 314				
<hr/>					
RESULTS					
2					
P05559					
Hypothetical protein ESPF6 (imported) - Arabidopsis thaliana					
C:Species:	Arabidopsis thaliana				
C>Date:	02-Mar-2001	Sequence revision 02-Mar-2001	textL change 31-Mar-2001		
C:Accession:	F96559				
R:Author(s):	Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso				
Chitt, C.W.; Chung, M.K.; Conn, L.F.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,					
ansen, M.P.; Hughes, B.; Hulzar, L.					
A:PubMed:	10616-820,	2000			
C.A.I., J.H., Li, Y., Liu, J.L., Jenkins, J., Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,					
Rizzo, M.; Rooney, T.; Rowley, D.; Sakono, H.; Liu, Z.A.; Luroso, J.S.; Melli, R.; Metzler					
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.					
A>Title:	Sequence and analysis of chromosome 1 of the plant Arabidopsis.				
A:Reference number:	A86141; MUID:21016719				
A:Accession:	I96559				
A:Status:	partial				
A:Molecule type:	DNA				
A:Residues:	1-730 <STO>				
<hr/>					
Genefiles:					
A:Cross-references: GB:AEO05173; NID:g2220464; PION:AMD12691.1; GSPDB:GM00141					
<hr/>					

Db 93 SYDSNMV 99

RESULT 7

Probable alpha-amyase (EC 3.2.1.1) - Clostridium acetobutylicum (fragment)
 C:Accession: F31837
 C:Date: 23-Oct-1999 #sequence_revision 22-Jan-1999 #text_change 22-Jun-1999
 R:Character: U.; Duerte, P.
 J. Bacteriol. 172, 6907-6918, 1990
 A>Title: Cloning, sequencing, and molecular analysis of the acetate decarboxylase g
 A:Reference number: A37837; MUID:91072241
 A:Accession: B37837
 A:Status: Translation not shown
 A:Molecule type: DNA
 A:Residues: 1469 <GEN>
 A:Cross-references: GB:M53392; GB:M34078; NID:g144708; PDB:AAA63759.1; PDB:g144709
 C:Superfamily: alpha-amyase, subtilis type: alpha-amyase core homology
 C:Keywords: glycosidase; hydrolase

Query Match 82.1%; Score 32; DB 2; Length 469;
 Best Local Similarity 85.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YDSSNMV 8

Db 286 YDSSNMV 292

RESULT 8

Pept. Protein - Staphylococcus epidermidis
 C:Species: Staphylococcus epidermidis
 C:Accession: S66531
 R:Kleber, C.; Berbaum, C.; Heidrich, C.; Reiss, M.; Sueling, J.; Iglesias-Wind, M.I.; Ken
 Bur. J. Biochem. 232, 478-489, 1995
 A>Title: Nucleotide sequence of the lambdoid Pept biosynthetic gene cluster and funct
 A:Reference number: S66531; MUID:96035882
 A:Accession: S66531
 A:Status: Translation not shown
 A:Molecule type: DNA
 A:Residues: 1571 <GEN>
 A:Cross-references: EMBL:249865; NID:g945014; PDB:CAM90021.1; PDB:g945015
 C:Genetics:
 A:Gene: Pept
 C:Superfamily: Escherichia coli ABC transporter mlaA; ATP-binding cassette homology
 C:Species: ATP; nucleotide binding: P-loop
 F:348-541
 F:365-372/Region: nucleotide-binding motif A (P-loop)

Query Match 82.1%; Score 32; DB 2; Length 571;
 Best Local Similarity 75.0%; Pred. No. 51;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SYDSNMV 8

Db 341 SYDSNMV 348

RESULT 9

hypothetical protein F11C1.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 A:Accession: T07062
 R:Palmer, S.
 Submitted to the EMBL Data Library, September 1995
 A:Reference number: Z19321

A:Accession: T20762
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1130 <MID>
 A:Cross-references: EMBL:Z54270; PDB:CAM91026.1; GSPDB:GN00028; CESP:F11C1.2
 A:Genetics: clon. source: clone F11C1
 A:Gene: CESP:F11C1.2
 A:Map position: X
 A:Introns: 23/3; 89/1

Query Match 75.5%; Score 31; DB 2; Length 130;
 Best Local Similarity 85.7%; Pred. No. 7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDSNMV 7

Db 68 SYDSNMV 74

RESULT 10

A30154
 Ige receptor alpha chain precursor - rat
 N:Alternate names: FC-epsilon R alpha chain precursor
 C:Species: Rattus norvegicus (Norway rat)
 C:Accession: Oct1997 #sequence_revision 18-Oct-1999 #text_change 21-Jan-2000
 R:Ritz, P.T.; Albrandt, K.; Robertso, J.W.
 Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988
 A>Title: cDNA heterogeneity suggests structural variants related to the high-affinity
 A:Reference number: A94203; MUID:88289772
 A:Accession: C31327
 A:Status: Translation not shown
 A:Molecule type: mRNA
 A:Residues: 1245 <GEN>
 A:Cross-references: GB:M21622; GB:J03811
 A:Experimental source: basophilic leukemia cell line, clone R3-4
 A:Accession: A31327
 A:Molecule type: mRNA
 A:Residues: 21245 <LIT>
 A:Cross-references: GB:M21622; NID:g204109; PDB:AAA41146.1; PDB:g204110; GB:J03811
 A:Experimental source: basophilic leukemia cell line
 R:Shimizu, A.; Repler, I.; Benfey, P.N.; Bechtel, E.H.; Stengelin, R.P.; Leder, P.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
 A>Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characteri
 A:Reference number: A94191; MUID:88158102
 A:Accession: A30154
 A:Molecule type: mRNA
 A:Residues: 21245 <GEN>
 A:Cross-references: GB:M21622; NID:g205332; PDB:AAA41582.1; PDB:g205332
 R:Kliet, J.P.; Metzger, H.; Haxl, J.; Kochen, J.
 Biochemistry 26, 4605-4610, 1987
 A>Title: A cDNA presumptively coding for the alpha subunit of the receptor with high
 A:Reference number: A27116; MUID:88024987
 A:Accession: A27116
 A:Molecule type: mRNA
 A:Residues: 21245 <GEN>
 A:Cross-references: GB:M21622; NID:g205332; PDB:AAA41582.1; PDB:g205332
 R:Repler, I.; Shimizu, A.; Leder, P.
 J. Biol. Chem. 264, 5912-5915, 1989
 A>Title: The gene for the rat mast cell high affinity Ige receptor alpha chain. struc
 A:Reference number: I55304; MUID:89174653
 A:Accession: I55304
 A:Status: Translation not shown
 A:Molecule type: DNA
 A:Residues: 116 <RES>
 A:Cross-references: GB:M25334; NID:g341335; PDB:AAA74562.1; PDB:g556391
 C:Superfamily: Fc gamma receptor II; Immunoglobulin homology
 C:Keywords: Immunoglobulin receptor; transmembrane protein
 F:1123/Domain: signal sequence #status predicted <Sig>
 F:142-93/Domain: Ige receptor alpha chain #status predicted <NAT>
 F:142-93/Domain: Immunoglobulin homology <IMM>

Query Match 79.5% Score 31: DB 2: Length 245:
 Best Local Similarity 71.4% Pred. No. 34:
 Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:
 Oy 1 YDSSNV 7
 111111:
 Db 153 SFDSNV 159

RESULT 11
 G84781
 hypothetical protein AL2936540 (imported) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: J04584; G23734
 R:Bio X: Kaul, S.; Bounieley, S.D.; Shee, T.P.; Benito, M.I.; Tom, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Motil, K.S.; Conlin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
 Euser, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venturi,
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Residues: 1-249 <STO>
 A:Molecule type: DNA
 A:Status: preliminary
 A:Cross-references: GB:AE002093; NID:94581152; PIDN:AMD24536.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AL2936540
 A:Map position: 2

Query Match 79.5% Score 31: DB 2: Length 249:
 Best Local Similarity 71.4% Pred. No. 35:
 Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:
 Oy 1 YDSSNV 7
 111111:
 Db 187 SFDSNV 193

RESULT 12
 T15520
 hypothetical protein C15H9.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
 C:Accession: T15520
 R:Bentley, D.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid C15H9.
 A:Reference number: T15520
 A:Residues: 1-218304
 A:Status: preliminary
 A:Molecule type: DNA
 A:Cross-references: EMBL:056965; NID:91945492; PID:91293841; PIDN:AA52662.1; GSPDB:GN00
 C:Genetics: CESP:C15H9.2
 A:Map position: X
 A:Indels: 16/3: 40/2: 78/3: 109/2: 137/3: 192/1: 244/3

Query Match 79.5% Score 31: DB 2: Length 261:
 Best Local Similarity 85.7% Pred. No. 37:
 Matches 6: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
 Oy 2 YDSSNV 8
 111111:
 Db 122 SFDSNV 128

RESULT 13.
 JC4584

Insulin-like growth factor binding protein-5 precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
 C:Accession: JC4584; G23734
 R:White, M.E.; Diao, R.; Bachway, M.R.; Mickelson, J.; Dayton, W.R.
 Blochem. Biophys. Res. Commun. 215:155-160, 1995
 A:Reference number: JC4584; MUID:96136509
 A:Accession: JC4584

A:Molecule type: mRNA
 A:Residues: 1-271 <MHI>
 A:Cross-references: GB:041340; NID:91173906; PIDN:AA87855.1; PID:911173907
 A:Experimental source: skeletal muscle
 A:Ethical approval: 5938-948, 1991
 A:Title: Isolation and molecular cloning of insulin-like growth factor-binding prot
 A:Reference number: A23734; MUID:92049376
 A:Accession: G23734
 A:Molecule type: protein
 A:Residues: 30-25; X:127-28; Y:30-36; Y:38-39 <SWI>
 A:Cross-references: EMBL:056965; NID:91945492; PID:91293841; PIDN:AA52662.1; GSPDB:GN00139
 A:Status: preliminary
 A:Molecule type: protein
 A:Cross-references: EMBL:056965; NID:91945492; PID:91293841; PIDN:AA52662.1; GSPDB:GN00139
 C:Genetics: CESP:F28G4.2
 A:Map position: 5
 A:Indels: 25/3: 49/3: 79/3: 173/3: 233/3: 324/2

Query Match 79.5% Score 31: DB 2: Length 271:
 Best Local Similarity 85.7% Pred. No. 38:
 Matches 6: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
 Oy 1 YDSSNV 7
 111111:
 Db 264 SFDSNV 270

RESULT 14
 T21513
 hypothetical protein F28G4.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21513
 R:Wall, M.
 submitted to the EMBL data library, March 1997
 A:Reference number: T21513
 A:Accession: T21513
 A:Status: preliminary
 A:Molecule type: translated from GB/EMBL/DBJ
 A:Residues: 1-3174 <WLI>
 A:Cross-references: EMBL:293381; PIDN:CA807605.1; GSPDB:GN00023; CESP:F28G4.2
 A:Experimental source: clone F28G4
 C:Genetics:
 A:Gene: CESP:F28G4.2
 A:Map position: 5
 A:Indels: 25/3: 49/3: 79/3: 173/3: 233/3: 324/2

Query Match 79.5% Score 31: DB 2: Length 374:
 Best Local Similarity 100.0% Pred. No. 54:
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Oy 2 YDSSNV 7
 111111:
 Db 80 YDSSNV 85

RESULT 15
 A70735
 hypothetical protein RV3712 - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: A70705
 R:Colet, S.T.; Brosch, R.; Parthill, J.; Gardner, T.; Church, C.; Harris, D.; Gordon, S.
 ; Comor, R.; Davies, R.; Devlin, K.; Felipelli, T.; Gentles, S.; Hamilton, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Fuller, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitlead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Accession: A70705; A70500; M01D:98295987
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-413 <COL>
 A:Cross-references: GB:AL022121; GB:AL123456; M1D:g3261559; PIDN:CAA18034.1; PID:e126457
 A:Experimental source: strain H37Rv
 A:Gene: NV3712

Query Match 79.5%; Score 31; DB 2; Length 413;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 SYDSSNV 8
 :|||||||
 Db 174 AYDSPNV 181

Search completed: November 19, 2001, 08:14:24
 Job time: 137 sec

THIS PAGE BLANK (USPTO)


```

OY      1 SYSSSNV 8
      1:|||||
Db      184 YDSSNV 191

RESULT 2
LVB6_HUMAN STANDARD: PRT: 112 AA.
ID P01722:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
IG LAMBDA CHAIN V-VI REGION NIG-48.
OS Homo sapiens (human).
OC Mammalia: Primates: Catarrhini: Hominoidea: Hominidae: Homo.
NC MBL_TaxID=9606;
CX [1]
RP SEQUENCE.
RA MEDLINE=80094390; PubMed=118171;
RA Takahashi N., Takayasu T., Isobe T., Shiroda T., Okuyama T.,
RA Shimizu A.,
RA "A preliminary study on the structure of the light chains of human
RA immunoglobulins. II. Assignment of a new subgroup. ";
RL J. Biochem. 86:1523-1535(1979).
CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR HSP: A01991; LSHU48.
DR HSP: P01703; YEAB.
DR INTERPRO: IPR003006;
DR SWISS-PROT: P01703;
DR Immunoglobulin V region; Bence-Jones protein.
FT NON_TER 112 112
SQ SEQUENCE 112 AA: 1152 MW: CPEBA30/BC527A384 CRC64:

Query Match
Best Local Similarity 82.1%: Score 32; DB 1; Length 112;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 SYSSSNV 7
      1:|||||
Db      93 YDSSNV 99

RESULT 3
COAA_BP1F1 STANDARD: PRT: 460 AA.
ID O80297:
AC O80297:
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DR BACTERIOPHAGE T1.
OS Bacteriophage T1.
OC Viruses: ssDNA viruses: Inoviridae: Inovirus.
NC MBL_TaxID=10868;
CX [1]
RP SEQUENCE FROM N.A.
RA "DNA sequence of the filamentous phage T1. ";
RA Submitted (OCT-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: COAT PROTEIN A IS NECESSARY FOR ADSORPTION OF THE VIRION
CC ONTO THE P-PILUS OF THE HOST CELL. (BY SIMILARITY).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL database.
CC The Swiss Institute of Bioinformatics and the EMBL database have no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC

```

```

DR EMBL: U02303; AAC62155.1;
KW Phage recognition; Coat protein; Signal.
FT SIGNAL 19
FT CHAIN 20 460 COAT PROTEIN A.
SQ SEQUENCE 460 AA: 48790 MW: 9AD651968C715AB2 CRC64:

Query Match
Best Local Similarity 85.7%: Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 SYSSSNV 7
      1:|||||
Db      229 YDSSNV 235

RESULT 4
AMY_C10AB STANDARD: PRT: 469 AA.
ID P23671:
AC P23671:
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE PUTATIVE ALPHA-AMYLASE (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
DE GLUCANOHYDROLASE) (FRAGMENT).
OS Clostridium acetobutylicum.
OC Bacteria: Firmicutes: Bacillus/Clostridium group: Clostridiaceae;
OC Clostridium.
CX MBL_TaxID=1488;
CX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DSM 792;
RC MEDLINE=9107241; PubMed=2254264;
RA Gerischer U., Duerte P.;
RA "Cloning, sequencing, and molecular analysis of the acetate
RA decarboxylase gene (acdc) from Clostridium acetobutylicum. ";
RL J. Biol. Chem. 267:4500-4506(1992).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL database.
CC The European Bioinformatics Institute has no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X146375.1;
DR EMBL: X146375.1;
DR HYDROLASE: Glycosylase; Carbohydrate metabolism.
FT NON_TER 1 1
SQ SEQUENCE 469 AA: 50870 MW: DB186702D9B01572 CRC64:

Query Match
Best Local Similarity 85.7%: Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      2 YDSSNV 8
      1:|||||
Db      286 YDSSNV 292

RESULT 5
FCBL_PAT STANDARD: PRT: 245 AA.
ID FCBL_PAT
AC P12371:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```


Query Match 79.5% Score 21. PB 1: Length 272:
 Local Similarity 83.7% ID: 15
 Matches 6: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

1 YDSSNV 7
 1:|||||
 Db 264 SPROSNV 270

RESULT 7
 SER3_DROME STANDARD: PRT: 272 AA.

AC P12707: OYVAB8; 15
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-OCT-2000 (Rel. 10, Last sequence update)
 DT 01-OCT-2000 (Rel. 10, Last annotation update)
 D 01-OCT-2000 (Rel. 10, Last annotation update)
 CN SRR99DC OR SER3 OR CCI7951
 CC Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tenebrata; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephyrididae; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 CX
 RN SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 AC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Colinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutcliffe G.C., Morten Y.N., Chishti R.C., Chishti M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.C., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Adayani A., An H.-J., Andrews-Plannoch C., Baldwin D.,
 RA Baevens R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Boerova D., Botchan M.R., Bouck J., Brokstein P., Brotherton I.,
 RA Burke A.M., Cawley S., Dhillon C., Davenport L.B., Davies P.,
 RA Dodson K., Doup I.E., Doves M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Foster K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Giodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Hattis N.L., Heston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Krevitz S., Kulp D., Lai Z.,
 RA Lanko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshell A.,
 RA Mount S.M., Moy R., Murphy J., Murphy J., Nelson D., Pacht J.M.,
 RA Palazotto R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Tector C., Turner R., Venier E., Wang R.H., Wang X.,
 RA Wang Z.-T., Wassenaar T., Weisburger K.C., Wu D., Yang S.,
 RA Ye J., Yeh R.-P., Zverev J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RN "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN SEQUENCE OF 2185-2772 FROM N.A.
 RC STRAIN=AT44;
 AC MEDLINE=99219063; PubMed=2469005;
 RA Yun Y., Davis R.L.;
 RN "Levels of RNA from a family of putative serine protease genes are
 reduced in Drosophila melanogaster double mutants and are regulated by
 cyclic AMP";
 RL Mol. Cell. Biol. 9:692-700(1989).

CC CC
 CC -1- FUNCTION: ITS MAJOR FUNCTION MAY BE TO AID IN DIGESTION.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THE LARVAL GUT.
 CC -1- DEVELOPMENTAL STAGE: BEGAN TO APPEAR AT LATE EMBRYO STAGE AND
 CC CONTINUED TO INCREASE IN ABUNDANCE THROUGHOUT THE LARVAL STAGE.
 CC THEY ARE NOT PRESENT IN PUPAE BUT REAPPEARED IN THE ADULT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSTEIN FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-ebc.org/licenses/>
 CC or send an email to license@isb-ebc.org).
 CC EMBL: A6003771; AAF56973.1; -;
 CC EMBL: M24380; AAB02551.1; -;
 CC PIR: P50049; P50049.
 CC HSSP: P00760; 1A07; Ser99DC.
 CC Elybase: FB98003358; Ser99DC.
 CC Interpro: IPR001254; -;
 CC DR Pfam: PF00089; trypsin.1.
 CC DR PRINTS: P600722; CHYMOTRPSIN.
 CC DR PROSITE: PS00134; TRYPsin_HIS. 1.
 CC DR PROSITE: PS00135; TRYPsin_SER. 1.
 CC KW Hydrolase; Serine protease; Signal; zymogen; Multigene family.
 CC FT SIGNAL 1 17
 CC FT CHAIN 41 272
 CC FT ACT_SITE 84 84
 CC FT ACT_SITE 127 127
 CC FT ACT_SITE 222 222
 CC FT ACT_SITE 222 222
 CC FT DISULFID 69 85
 CC FT DISULFID 193 208
 CC FT DISULFID 239 256
 CC FT CONFLICT 212 212
 CC SEQUENCE 272 AA; 29620 MW; A61E9DE3AFC93AF CRC64;

Query Match 79.5% Score 21. PB 1: Length 272:
 Local Similarity 83.7% ID: 15
 Matches 6: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

2 YDSSNV 8
 1:|||||
 Db 171 YDSSNV 177

RESULT 8
 PRZN_RENSA STANDARD: PRT: 548 AA.

AC P55111; 34
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 10, Last annotation update)
 D 01-OCT-2000 (Rel. 10, Last annotation update)
 CN METALLOPROTEINASE PROTEIN (DC 3.4.21.-) (HBMOLYSIN).
 CC HLY
 CC Renibacterium salmoninarum.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Micrococcales; Micrococcaceae; Renibacterium.
 CC NCBI_TaxID=1646;
 RN SEQUENCE FROM N.A.
 RC STRAIN=AT44;
 AC MEDLINE=95400487; PubMed=7545509;
 RA Grayson T.B., Evenden A.J., Gilpin M.L., Martin K.L., Muon C.B.;
 RN "A gene from Renibacterium salmoninarum encodes a product which
 shows homology to bacterial zinc-metalloproteases";
 RL Microbiology 141:131-134(1995)
 CC -1- FUNCTION: KINETOGEN-LIKE ACTIVITY WITH HPMOLYTIC PROPERTIES.
 CC HEMOLYTIC ACTIVITY IS OBSERVED FROM 6 TO 37 DEGREES CELSIUS FOR

FT	MUTAGEN	532	532	R->A: 60% DECREASE OF ACTIVITY.
FT	MUTAGEN	537	537	R->A: NO CHANGE IN ACTIVITY.
FT	MUTAGEN	550	550	R->A: 83% DECREASE OF ACTIVITY.
FT	MUTAGEN	551	551	R->A: 93% DECREASE OF ACTIVITY.
FT	MUTAGEN	559	559	L->A: 95% DECREASE OF ACTIVITY.
FT	MUTAGEN	561	561	E->A: LOSS OF ACTIVITY.
FT	MUTAGEN	561	561	E->D: 65% DECREASE OF ACTIVITY.
FT	MUTAGEN	561	561	E->D: LOSS OF ACTIVITY.
FT	MUTAGEN	562	562	D->A: LOSS OF ACTIVITY.
FT	MUTAGEN	562	562	D->E: LOSS OF ACTIVITY.
FT	MUTAGEN	563	563	D->N: LOSS OF ACTIVITY.
FT	MUTAGEN	563	563	R->A: 94% DECREASE OF ACTIVITY.
FT	MUTAGEN	565	565	L->A: 95% DECREASE OF ACTIVITY.
FT	MUTAGEN	589	589	T->A: 70% DECREASE OF ACTIVITY.
FT	MUTAGEN	592	592	P->A: 70% DECREASE OF ACTIVITY.
FT	MUTAGEN	601	601	Q->A: LOSS OF ACTIVITY.
FT	MUTAGEN	601	601	Q->N: LOSS OF ACTIVITY.
FT	MUTAGEN	602	602	R->A: LOSS OF ACTIVITY.
FT	MUTAGEN	602	602	R->A: LOSS OF ACTIVITY.
FT	MUTAGEN	603	603	R->A: LOSS OF ACTIVITY.
FT	MUTAGEN	603	603	R->K: 57% DECREASE OF ACTIVITY.
FT	MUTAGEN	604	604	R->K: LOSS OF ACTIVITY.
FT	MUTAGEN	604	604	R->A: LOSS OF ACTIVITY.
FT	MUTAGEN	604	604	R->K: LOSS OF ACTIVITY.
FT	MUTAGEN	605	605	W->A: LOSS OF ACTIVITY.
FT	MUTAGEN	605	605	W->Y: LOSS OF ACTIVITY.
FT	MUTAGEN	607	607	R->A: 95% DECREASE OF ACTIVITY.
FT	MUTAGEN	607	607	R->A: 95% DECREASE OF ACTIVITY.
SDSOURCE		963 Aa:	109881 Mw:	404A4A8A7C0B65B5B CAC04:

Query Match	79.5%	Score 31;	DB 1;	Length 963;
Best Local Similarity	85.7%	Pred. No. 62;		
Matches	6;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0

QY	1	SYDSSNV	7
Db	47	SYDQSNV	53

DE	RESULT	10	CTA2_1BACCI	STANDARD:	PRT:	964 AA.
AC	ID	CTA2_1BACCI				
AD	P10873					
AE	15-JUL-1998	(Rel. 36, Created)				
AF	15-JUL-1998	(Rel. 36, Last sequence update)				
AG	15-JUL-1998	(Rel. 36, Last annotation update)				
DE	CYCLOLIMONATOOLISACCHARIDE GLUCONOTANSFERASE	PRECURSOR (EC 2.4.1.7)				

CC 05. *Bacillus circulans*.
CC 06. Bacteria; Firmicutes; Bacillus/Clostridium group;
CC 07. *Bacillus*; *Staphylococcus* group; *Bacillus*.
CC 08. NCBI_TaxID=1397;
CC 09. [1]
CC 10. SEQUENCE FROM N.A.
CC 11. STRAIN=U-155.
CC 12. STRAIN=U-155.
CC 13. STRAIN=U-155.
CC 14. STRAIN=U-155.
CC 15. Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC 16. -1- FUNCTION. PRODUCES CYCLOSTOLICACID/CLARIDEX FROM DEXTRAN.
CC 17. -1- SIMILARITY. BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
CC 18. -1-
CC 19. -1-
CC 20. -1-
CC 21. -1-
CC 22. -1-
CC 23. -1-
CC 24. -1-
CC 25. -1-
CC 26. -1-
CC 27. -1-
CC 28. -1-
CC 29. -1-
CC 30. -1-
CC 31. -1-
CC 32. -1-
CC 33. -1-
CC 34. -1-
CC 35. -1-
CC 36. -1-
CC 37. -1-
CC 38. -1-
CC 39. -1-
CC 40. -1-
CC 41. -1-
CC 42. -1-
CC 43. -1-
CC 44. -1-
CC 45. -1-
CC 46. -1-
CC 47. -1-
CC 48. -1-
CC 49. -1-
CC 50. -1-
CC 51. -1-
CC 52. -1-
CC 53. -1-
CC 54. -1-
CC 55. -1-
CC 56. -1-
CC 57. -1-
CC 58. -1-
CC 59. -1-
CC 60. -1-
CC 61. -1-
CC 62. -1-
CC 63. -1-
CC 64. -1-
CC 65. -1-
CC 66. -1-
CC 67. -1-
CC 68. -1-
CC 69. -1-
CC 70. -1-
CC 71. -1-
CC 72. -1-
CC 73. -1-
CC 74. -1-
CC 75. -1-
CC 76. -1-
CC 77. -1-
CC 78. -1-
CC 79. -1-
CC 80. -1-
CC 81. -1-
CC 82. -1-
CC 83. -1-
CC 84. -1-
CC 85. -1-
CC 86. -1-
CC 87. -1-
CC 88. -1-
CC 89. -1-
CC 90. -1-
CC 91. -1-
CC 92. -1-
CC 93. -1-
CC 94. -1-
CC 95. -1-
CC 96. -1-
CC 97. -1-
CC 98. -1-
CC 99. -1-
CC 100. -1-
CC 101. -1-
CC 102. -1-
CC 103. -1-
CC 104. -1-
CC 105. -1-
CC 106. -1-
CC 107. -1-
CC 108. -1-
CC 109. -1-
CC 110. -1-
CC 111. -1-
CC 112. -1-
CC 113. -1-
CC 114. -1-
CC 115. -1-
CC 116. -1-
CC 117. -1-
CC 118. -1-
CC 119. -1-
CC 120. -1-
CC 121. -1-
CC 122. -1-
CC 123. -1-
CC 124. -1-
CC 125. -1-
CC 126. -1-
CC 127. -1-
CC 128. -1-
CC 129. -1-
CC 130. -1-
CC 131. -1-
CC 132. -1-
CC 133. -1-
CC 134. -1-
CC 135. -1-
CC 136. -1-
CC 137. -1-
CC 138. -1-
CC 139. -1-
CC 140. -1-
CC 141. -1-
CC 142. -1-
CC 143. -1-
CC 144. -1-
CC 145. -1-
CC 146. -1-
CC 147. -1-
CC 148. -1-
CC 149. -1-
CC 150. -1-
CC 151. -1-
CC 152. -1-
CC 153. -1-
CC 154. -1-
CC 155. -1-
CC 156. -1-
CC 157. -1-
CC 158. -1-
CC 159. -1-
CC 160. -1-
CC 161. -1-
CC 162. -1-
CC 163. -1-
CC 164. -1-
CC 165. -1-
CC 166. -1-
CC 167. -1-
CC 168. -1-
CC 169. -1-
CC 170. -1-
CC 171. -1-
CC 172. -1-
CC 173. -1-
CC 174. -1-
CC 175. -1-
CC 176. -1-
CC 177. -1-
CC 178. -1-
CC 179. -1-
CC 180. -1-
CC 181. -1-
CC 182. -1-
CC 183. -1-
CC 184. -1-
CC 185. -1-
CC 186. -1-
CC 187. -1-
CC 188. -1-
CC 189. -1-
CC 190. -1-
CC 191. -1-
CC 192. -1-
CC 193. -1-
CC 194. -1-
CC 195. -1-
CC 196. -1-
CC 197. -1-
CC 198. -1-
CC 199. -1-
CC 200. -1-
CC 201. -1-
CC 202. -1-
CC 203. -1-
CC 204. -1-
CC 205. -1-
CC 206. -1-
CC 207. -1-
CC 208. -1-
CC 209. -1-
CC 210. -1-
CC 211. -1-
CC 212. -1-
CC 213. -1-
CC 214. -1-
CC 215. -1-
CC 216. -1-
CC 217. -1-
CC 218. -1-
CC 219. -1-
CC 220. -1-
CC 221. -1-
CC 222. -1-
CC 223. -1-
CC 224. -1-
CC 225. -1-
CC 226. -1-
CC 227. -1-
CC 228. -1-
CC 229. -1-
CC 230. -1-
CC 231. -1-
CC 232. -1-
CC 233. -1-
CC 234. -1-
CC 235. -1-
CC 236. -1-
CC 237. -1-
CC 238. -1-
CC 239. -1-
CC 240. -1-
CC 241. -1-
CC 242. -1-
CC 243. -1-
CC 244. -1-
CC 245. -1-
CC 246. -1-
CC 247. -1-
CC 248. -1-
CC 249. -1-
CC 250. -1-
CC 251. -1-
CC 252. -1-
CC 253. -1-
CC 254. -1-
CC 255. -1-
CC 256. -1-
CC 257. -1-
CC 258. -1-
CC 259. -1-
CC 260. -1-
CC 261. -1-
CC 262. -1-
CC 263. -1-
CC 264. -1-
CC 265. -1-
CC 266. -1-
CC 267. -1-
CC 268. -1-
CC 269. -1-
CC 270. -1-
CC 271. -1-
CC 272. -1-
CC 273. -1-
CC 274. -1-
CC 275. -1-
CC 276. -1-
CC 277. -1-
CC 278. -1-
CC 279. -1-
CC 280. -1-
CC 281. -1-
CC 282. -1-
CC 283. -1-
CC 284. -1-
CC 285. -1-
CC 286. -1-
CC 287. -1-
CC 288. -1-
CC 289. -1-
CC 290. -1-
CC 291. -1-
CC 292. -1-
CC 293. -1-
CC 294. -1-
CC 295. -1-
CC 296. -1-
CC 297. -1-
CC 298. -1-
CC 299. -1-
CC 300. -1-
CC 301. -1-
CC 302. -1-
CC 303. -1-
CC 304. -1-
CC 305. -1-
CC 306. -1-
CC 307. -1-
CC 308. -1-
CC 309. -1-
CC 310. -1-
CC 311. -1-
CC 312. -1-
CC 313. -1-
CC 314. -1-
CC 315. -1-
CC 316. -1-
CC 317. -1-
CC 318. -1-
CC 319. -1-
CC 320. -1-
CC 321. -1-
CC 322. -1-
CC 323. -1-
CC 324. -1-
CC 325. -1-
CC 326. -1-
CC 327. -1-
CC 328. -1-
CC 329. -1-
CC 330. -1-
CC 331. -1-
CC 332. -1-
CC 333. -1-
CC 334. -1-
CC 335. -1-
CC 336. -1-
CC 337. -1-
CC 338. -1-
CC 339. -1-
CC 340. -1-
CC 341. -1-
CC 342. -1

FT	CHAIN	31	964	CYCLISOMLITOOIGDSACCHARIDE
PT				GIUDONTNENRSEAE
SQ	SEQUENCE	964 AA:	107208 NM:	8849CDDC5E2DE9A68 CRC64:
Query Match		79.5%	Score 31:	DB 1: Length 964
Best Local		Similarity 100.0%	Pred. No. 62:	
Matches		6: Conservative	0: Mismatches	0: Indels

Oy	1	SYDSSN	6
Db	521	SYDSSN	526

RESULT	11		
AC	CDS/CDS	STANDARD:	PRT: 332 AA.
AC	O15831:		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DR	TRANSCRIPTION REGULATORY PROTEIN REGA.		
DN	RECA OR REGA.		
GN	Regulatory protein Rea		
OS	Bacillus anthracis		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;		
CC	Clostridium.		
NCBI	taxid=1488;		
RN	[1]		
RF	SEQUENCE FROM N.A.		
RC	STRAIN=262;		
RL	MEDLINE=7591448, PubMed=7536989;		
RT	"Bacillus S. Stammesleim J.D. Reid S.J., Woods D.R. ;		
RX	"A.Clostridium acetobutylicum regulator gene (regA) affecting amylose		
RE	production in Bacillus subtilis.";		
RE	Microbiology 141:989-996(1995).		
CC	-1- FUNCTION: INVOLVED IN THE REGULATION OF AMYLASE PRODUCTION.		
CC	-1- SIMILARITY: BELONGS TO THE LACT FAMILTY OF TRANSCRIPTIONAL		
CC	REGULATORS.		
CC	-----		
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and The EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way repack-		
CC	aged or modified and this statement is not removed, changed or extended by any subsequent		
CC	entries requires a license (see http://www.isdb.ch/announce/)		
CC	-----		
CC	EMBL: L14685; AAA23275.1;"		
DR	HSSP: P15039; IPHY.		
DR	InterPro: IPR000843; "		
DR	InterPro: IPR001761; "		
DR	Plan: PF00322; beta_lap_IIIc-like; 1.		
DR	PRINTS: PF00326; HTLLACT.		
DR	PRINTS: PS00356; HTN_LACTI_FAMILY; 1.		
DR	Transcription regulation; DNA-binding.		
KM	DNA_BIND	5 24	H-H motif (POTENTIAL);
SO	SEQUENCE	332 AA; 37260 MW; 27CB852F9BB5B07 CR6d6;	

Query Match 76.9%; Score 30; DB 1; Length 332;

[illegible]

RESULT	12	
YN8H_YEAST		
ID	YN8H_YEAST	STANDARD;
AC	P53729;	PRT; 429 AA

Query Match	Best Local Similarity	79.5%	Score 31:	DB 1:	Length 963:				
Matches	6:	Conservative	0:	Mismatches	1:	Indels	0:	Gaps	0:
Db	47	SYDSNV 53							
1	SYDSNV 7								
2	SYDSNV 7								
3	SYDSNV 7								
4	SYDSNV 7								
5	SYDSNV 7								
6	SYDSNV 7								
7	SYDSNV 7								
8	SYDSNV 7								
9	SYDSNV 7								
10	SYDSNV 7								
11	SYDSNV 7								
12	SYDSNV 7								
13	SYDSNV 7								
14	SYDSNV 7								
15	SYDSNV 7								
16	SYDSNV 7								
17	SYDSNV 7								
18	SYDSNV 7								
19	SYDSNV 7								
20	SYDSNV 7								
21	SYDSNV 7								
22	SYDSNV 7								
23	SYDSNV 7								
24	SYDSNV 7								
25	SYDSNV 7								
26	SYDSNV 7								
27	SYDSNV 7								
28	SYDSNV 7								
29	SYDSNV 7								
30	SYDSNV 7								
31	SYDSNV 7								
32	SYDSNV 7								
33	SYDSNV 7								
34	SYDSNV 7								
35	SYDSNV 7								
36	SYDSNV 7								
37	SYDSNV 7								
38	SYDSNV 7								
39	SYDSNV 7								
40	SYDSNV 7								
41	SYDSNV 7								
42	SYDSNV 7								
43	SYDSNV 7								
44	SYDSNV 7								
45	SYDSNV 7								
46	SYDSNV 7								
47	SYDSNV 7								
48	SYDSNV 7								
49	SYDSNV 7								
50	SYDSNV 7								
51	SYDSNV 7								
52	SYDSNV 7								
53	SYDSNV 7								
54	SYDSNV 7								
55	SYDSNV 7								
56	SYDSNV 7								
57	SYDSNV 7								
58	SYDSNV 7								
59	SYDSNV 7								
60	SYDSNV 7								
61	SYDSNV 7								
62	SYDSNV 7								
63	SYDSNV 7								
64	SYDSNV 7								
65	SYDSNV 7								
66	SYDSNV 7								
67	SYDSNV 7								
68	SYDSNV 7								
69	SYDSNV 7								
70	SYDSNV 7								
71	SYDSNV 7								

RT "A *Clostridium acetobutylicum* regulator gene (*rega*) affecting amylase production in *Bacillus subtilis*.";
RT Microbiology 141:989-995(1995)

CC - FUNCTION: 1
CC - SIMILARITY: 1
CC REGULATORS.

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation, no
CC the European Bioinformatics Institute, and its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL, L14685; AAK23275.1; -
DR HSSP; L15012600043; -
DR

[illegible]

RESULT	12	
YN8H_YEAST		
ID	YN8H_YEAST	STANDARD;
AC	P53729;	PRT; 429 AA

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:25:04 ; Search time 81.19 Seconds
(without adjustments)

Title: US-09-610-118-66

Sequence: 1 SYDSSNVV 8

Scoring table: BLOSUM62

1300000000

Total number of hits satisfying chosen parameters: 425026

```
Minimum DB seq length: 0
```

[illegible]

Listing first 45 summaries

```

1: SPtREMBL.16:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebr:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.unclassified
13: sp.vertebrata
14: sp.virus:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	33	84.6	660	10	P93658	P93658 brassica n
2	33	84.6	730	10	O92823	O92823 arabidopsi
3	33	84.6	730	2	O92823	O92823 arabidopsi
4	33	84.6	1945	5	O56681	O56681 dirosophila
5	33	84.6	1945	5	O94931	O94931 dirosophila
6	32	82.1	506	5	O9N314	O9N314 caenorhabd
7	32	82.1	531	5	O9VDD3	O9VDD3 dirosophila
8	32	82.1	537	5	P91310	P91310 caenorhabd
9	32	82.1	542	5	O9Y9K0	O9Y9K0 dirosophila
10	32	82.1	571	2	O54121	O54121 staphylococ
11	32	82.1	760	2	O9S429	O9S429 clostridium
12	32	82.1	1938	2	P70593	P70593 bacillus s
13	31	79.5	1315	5	O9Y9G9	O9Y9G9 dirosophila
14	31	79.5	1315	5	O9Y9G9	O9Y9G9 dirosophila
15	31	79.5	192	5	O9Y8A2	O9Y8A2 dirosophila
16	31	79.5	261	10	O9S0Q4	O9S0Q4 arabidopsi
17	31	79.5	261	5	O18030	O18030 caenorhabd
18	31	79.5	274	5	O17086	O17086 anoplasis
19	31	79.5	374	5	O17852	O17852 caenorhabd

1	31	79.5	41.1	2	068342	Bacillus
2	31	79.5	40.2	2	068522	mycoelast
3	31	79.5	41.3	2	056767	mycoelast
4	31	79.5	41.3	2	056767	mycoelast
5	31	79.5	51.3	3	059893	candidate alt
6	31	79.5	66.9	11	050872	Oryziz
7	31	79.5	72.7	10	039715	Oryziz
8	31	79.5	72.7	10	039715	arabidops
9	31	79.5	78.3	10	004196	arabidops
10	31	79.5	86.2	3	013144	aspergill
11	31	79.5	86.2	3	013144	aspergill
12	30	76.9	126.1	14	059585	felline cal
13	30	76.9	127.1	14	059585	felline cal
14	30	76.9	14.5	6	P79318	human pap
15	30	76.9	14.5	6	P79318	human pap
16	30	76.9	22.9	2	045551	isobacilli
17	30	76.9	27.0	10	005858	arabidops
18	30	76.9	33.1	14	068443	paramusci
19	30	76.9	33.1	14	068443	paramusci
20	30	76.9	34.3	4	059809	Oryziz
21	30	76.9	35.5	3	059473	homio sapler
22	30	76.9	35.5	3	059473	homio sapler
23	30	76.9	35.4	10	059594	arabidops
24	30	76.9	35.8	5	044553	caneracard
25	30	76.9	42.8	5	005455	caneracard
26	30	76.9	42.8	5	005455	caneracard
27	30	76.9	46.6	10	065187	arabidops
28	30	76.9	47.2	4	059809	homio sapler
29	30	76.9	51.3	5	059718	droscophila

ALIGNMENTS

```

RESULT      1
ID           P93658      PRELIMINARY:      PRT:      680 AA.
AC           P93658
DC           P93658;1997 (TREMBLrel. 03, Created)
DT           01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT           01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE           JASMONATE INDUCIBLE PROTEIN.
OS           Brassica napus (rape).
OC           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC           Magnoliopsida; Brassicales; eudicots; Rosidae; eurosids II;
OC           Brassicaceae; Brassica.
OX           NCBI_TaxId=3708;
RN           [1]
RS           SEQUENCE FROM N. A.
RC           STRAIN=GLOBAL;
RC           GenH.N., Brandt, A.
RA           GenBank/EMBL/GenBank/DBJ databases.
DR           EMBL: Y11483; CAZ62271.1; -.
DR           HSSP: P18670; LJCX.
DR           Mandel: 14859; Brana:2387;14859.
DR           InterPro: IPR001229; -.
DR           Pfam: PF0119; Jcsc10; 4.
SQ           SEQUENCE      680 AA; 69397 MW;      8C00CF16C30CA1E2 CRC64;
Query Match      84.6%; Score 33; DB 10; Length 680;
Best Local Similarity      75.4%; Pred. No. 68;
Matches      2; Conservative      2; Mismatches      0; Indels      0; Gaps      0
OY           2 YSSNNV 8
Db           308 YSSNNI 314

RESULT      2
ID           P99023      PRELIMINARY:      PRT:      730 AA.
AC           P99023;
DC           09A023;
DT           01-MAY-1999 (TREMBLrel. 10, Created)
DT           01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT           01-MAY-2000 (TREMBLrel. 13, Last annotation update)

```

DE F5F19.6 PROTEIN.
GN Arabidopsis thaliana (Mouse-ear cross).
OS Arabidopsis thaliana: Embryophyta; Tracheophyta; Spermatophyta;
OC Malvaceae: Rosales: Malvaceae: core eudicots: Rosidae: eurosid II;
OX NCBI_TaxID=3702.
RN [1]
RP SEQUENCE FROM N.A.
RA Vaynskaia V.S., Schwartz J.R., Toriumi M., Yu G., Ienz C., Liu S.,
RA Blahut, Kremenetskaya I., Luros J., Gonzalez A., Altieri H., Araujo R.,
RA Kier C., Palm C., Foye J., Dunn P., Hansen N., Hultzer L.,
RA Ecker J.R., Pedersen M.A., Theologis A., Walker M., Davis R.W.,
RA "Arabidopsis thaliana chromosome 1 BAC F5f19 sequence."
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AC005216; AAC12691.1; -
DR HSP: P16870; JAC.
DR InterPro: IPR001236; -
DR Pfam: PF01419; Jaccalin; 3.
DR PROSITE: PS00325; CRYSTALLIN_BETACAMMA; UNKNOWN.1.
SO SEQUENCE 730 AA; 7399 MW; E432AF93BD5E CRC64;

Query Match 84.6%; Score 33; DB 10; Length 730;
Best Local Similarity 71.4%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 YSSSNV 8
DB 511 YSSSNV 517

RESULT 3
Q9PMF2 PRELIMINARY; PRT; 934 AA.
ID Q9PMF2
AC Q9PMF2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 15, Last annotation update)
DE PUTATIVE FORAMATE DEHYDROGENASE LARGE SUBUNIT (SERENOCYSTEINE
DE CONTAINING) (EC 1.2.1.2).
GN FOHA OR CJ1511.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC empty vector.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parthill J., Wren B.W., Mungall K., Kestley J.M., Churcher C.,
RA Barnham D., Chillingworth T., Davis R.M., Felvel J.T., Holtroyd S.,
RA O'Neill M.A., Rajendran A., Rutherford K.H., Van Vliet A.H.M.,
RA Mitchell S., Barrett B.G., Rutherford K.H., Van Vliet A.H.M.,
RA "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL: AL130781; CAB73932.1; -
DR InterPro: IPR001236; -
DR Pfam: PF01384; molycop_binding; 1.
DR PROSITE: PS00551; MOLYDOPTEIN_PROK_L; UNKNOWN.1.
DR PROSITE: PS00551; MOLYDOPTEIN_PROK_L; UNKNOWN.1.
SO SEQUENCE 934 AA; 103906 MW; 56138220BD643DA CRC64;

Query Match 84.6%; Score 33; DB 2; Length 934;
Best Local Similarity 63.5%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YSSSNV 8

DB 714 YSSSNV 721

RESULT 4
Q96681 PRELIMINARY; PRT; 1945 AA.
ID Q96681
AC Q96681
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PLEXIN A.
GN PLEXIN A.
OS Drosophila melanogaster (Fruit fly).
OC Insecta; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phlebotominae; Diptera; Euphymeria; Diptera; Brachycera; Muscomorpha;
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99051049; PubMed=9875845;
RA Winberg M.L., Noordermeer J.N., Tamagnone L., Comoglio P.M.,
RA "Plexin A is a neuronal semaphorin receptor that controls axon
RT guidance."
RL Cell 95:903-916(1998).
DR EMBL: AF106932; AAC09425.1; -
DR FlyBase: FBgn0025741; plexA.
DR InterPro: IPR001236; -
DR InterPro: IPR001236; -
DR InterPro: IPR001236; -
DR Pfam: PF01403; Sema; 2.
DR Pfam: PF01437; plexin_repeat; 3.
DR Pfam: PF01833; TIG; 3.
DR PROSITE: PS00264; SEMPRIN; UNKNOWN.1.
DR PROSITE: PS00264; SEMPRIN; UNKNOWN.1.
SO SEQUENCE 1945 AA; 218278 MW; 0903655980BDEP1 CRC64;

Query Match 84.6%; Score 33; DB 5; Length 1945;
Best Local Similarity 62.5%; Pred. No. 2,1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSSSNV 8
DB 1266 YSSSNV 1273

RESULT 5
Q9V491 PRELIMINARY; PRT; 1945 AA.
ID Q9V491
AC Q9V491
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PLEXIN A.
GN PLEXIN A.
OS Drosophila melanogaster (Fruit fly).
OC Insecta; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phlebotominae; Diptera; Euphymeria; Diptera; Brachycera; Muscomorpha;
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceoliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaralides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Braden R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Men K.H., Doyle G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Aotli J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Baeson K.M., Basu A., Baxter B.P., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.M., Bolch S.P., Bolintineanu D., Bolton E.S.,
 RA Borokova D., Botchan M.P., Butler H., Cadiot G., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke S., Dangel Z., Davis S.,
 RA DePablo J.B., Delcher A., Deng Z., Dey I., Dietz S.M.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Glöck A., Gong L., Green E.D., Gu Z., Guan P., Harris M.,
 RA Harris M.T., Harvey D., Heiman M., Hu Z., Huang J., Jarvis R.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idaguchi J.,
 RA Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Maitav A., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mount S.M., Moy M., Murphy B., Muzny D., Morris J., Moskaitis J.E.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nuskens D.R., Padgett M.O.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J.D., Puri V., Reese M.G.,
 RA Relnick K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E.C., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Stretz A., Tabor C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Xiao Q., Zheng L.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zhang X.H., Zhong F.N., Zhong G.M., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA The genome of *Drosophila melanogaster*.
 RL Science 287:2185-2196 (2001).
 DR EMBL: AEO03846; AAC59394.1;
 DR Flybase: Fg00025741; plexa.
 DR InterPro: IPR000215;
 DR InterPro: IPR001627;
 DR InterPro: IPR002165;
 DR InterPro: IPR002165;
 DR Pfam: PF01437; Plexin-repeat; 3.
 DR Pfam: PF01833; TIG: 3.
 DR Prosite: PS00284; SERPIN; UNKNOWN.1.
 DR SMART: SM00423; PSI: 1.
 SQ SEQUENCE 1945 AA: 218356 MW: 400320407083A745 CRC64;

Query Match 84.6%; Score 33; DB 5; Length 1945;
 Best Local Similarity 62.5%; Pred. No. 2; E=1e-02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 1266 STRESN1 1273

SYNOPSIS
 1 SYNOPSIS 8

RESULT 6
 ID 09N314 PRELIMINARY: PRT: 506 AA.
 DT 01-OCT-2000 (TREMBL:rel. 15, Created)
 DT 01-OCT-2000 (TREMBL:rel. 15, Last annotation update)
 DE Y51H7C.F PROTEIN.
 GN Y51H7C.F.
 OS Caenorhabditis elegans.
 OC Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Caenorhabditis.
 OX NCBI_TaxID=6233;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA MEDLINE=9065613; PubMed=9851916;
 RA None;

RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology." The C. elegans Sequencing Consortium.*
 RL Science 282:2012-2018(1998).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA MEDLINE=9065613;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024805; AAC59505.1;
 SQ SEQUENCE 506 AA: 57932 MW: B079349304A12DB CRC64;

Query Match 82.1%; Score 32; DB 5; Length 506;
 Best Local Similarity 65.7%; Pred. No. 62;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 257 SYDSTV 263

SYNOPSIS
 1 SYNOPSIS 7

RESULT 7
 ID 09V03 PRELIMINARY: PRT: 521 AA.
 AC 09V03;
 DT 01-MAY-2000 (TREMBL:rel. 13, Created)
 DT 01-MAY-2000 (TREMBL:rel. 13, Last sequence update)
 DE Y51H7C.F PROTEIN.
 GN Y51H7C.F.
 OS Caenorhabditis elegans.
 OC Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Caenorhabditis.
 OX NCBI_TaxID=6233;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA MEDLINE=9065613; PubMed=9851916;
 RA None;

RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology." The C. elegans Sequencing Consortium.*
 RL Science 282:2012-2018(1998).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA MEDLINE=9065613;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024805; AAC59505.1;
 SQ SEQUENCE 506 AA: 57932 MW: B079349304A12DB CRC64;

Query Match 82.1%; Score 32; DB 5; Length 506;
 Best Local Similarity 65.7%; Pred. No. 62;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 257 SYDSTV 263

SYNOPSIS
 1 SYNOPSIS 7

RESULT 7
 ID 09V03 PRELIMINARY: PRT: 521 AA.
 AC 09V03;
 DT 01-MAY-2000 (TREMBL:rel. 13, Created)
 DT 01-MAY-2000 (TREMBL:rel. 13, Last sequence update)
 DE Y51H7C.F PROTEIN.
 GN Y51H7C.F.
 OS Caenorhabditis elegans.
 OC Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Caenorhabditis.
 OX NCBI_TaxID=6233;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA MEDLINE=9065613; PubMed=9851916;
 RA None;

Query Match	82.18;	Score 32;	DB 5;	Length 527
-------------	--------	-----------	-------	------------

SO	SEQUENCE	542 AA; 61580 MW; 6D946885BEA57EB5 CRC64;
Query Match	82.1%;	Score 32; DB 5; Length 542

Best local similarity 85.7%; Pred. No. 88;

```

Matches 5: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 SYSSSNV 7
DB 95 YDSSSNV 101

RESULT 10
054121 PRELIMINARY; PRT; 571 AA.
ID 054121
AC 095429
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
PEPT.
GN Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Staphylococcus epidermidis.
OC NCBI_TaxID=1282,
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5;
RX MEDLINE=96035882; PubMed=7556197;
RA Meyer C., Bierbaum G., Heidrich C., Reis M., Suling J.,
RA "Staphylococcus M. Kempere, J. Molitor E., Sant H.G.;
RA "Staphylococcus M. Kempere, J. Molitor E., Sant H.G.;
RT Molecular analysis of the pepC biosynthetic gene cluster
RT and functional analysis of pepC and pepC. Evidence for a role of pepC
RT in biofilm formation."
RL Eur. J. Biochem. 232:478-489(1995).
-1- SIMILARITY: TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC
-1- TRANSPORTERS).
CC BMRB: 24966; CNA90021.1; -.
CC DR BMRB: 24966
CC DR InterPro: IPR001140; -.
CC DR InterPro: IPR003439; -.
CC DR InterPro: IPR003593; -.
CC DR Pfam: PF00064; ABC_tran: 1.
CC DR PROSITE: PS00023; ABC_TRANSPORTER: 1.
CC DR SMART: SM00382; AAA
CC DR ATP-binding; Transport.
CC KN
SQ SEQUENCE 571 AA; 64178 MW; 0AC37004CF86149 CRC64;

Query Match 82.1% Score 32; DB 2; Length 571;
Best Local Similarity 75.0% Pred. No. 94;
Matches 0; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 SYSSSNV 8
DB 341 YDSSSNV 348

RESULT 11
058429 PRELIMINARY; PRT; 760 AA.
ID 058429
AC 095429
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
ALPHA-AMYLASE PRECURSOR.
GN Amylase precursor.
OC Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC824
RT Sabathe F., Cornillot E., Croux C., Soucaille P.;

```

```

RT *Molecular characterization of amyP, a PSOL1 located gene coding the
RT major alpha-amylase of Clostridium acetobutylicum ATCC824, and its use
RT as a reporter system for strain degeneration."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR HSSP: P00691; A044702.1; -.
DR InterPro: IPR000461; -.
DR Pfam: PF00128; alpha-amylase: 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
FT SIGNAL
FT SIGNAL 1
FT CHAIN 45
FT SEQUENCE 760 AA; 1051467402321600 CRC64;

Query Match 82.1% Score 32; DB 2; Length 760;
Best Local Similarity 85.7% Pred. No. 13et02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 YDSSSNV 8
DB 577 YDSSSNV 583

RESULT 12
P70993 PRELIMINARY; PRT; 1938 AA.
ID P70993
AC P70983
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ALKALINE AMYLOPOLYLAMINASE.
OC Bacillus sp.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OC NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-1378;
RX MEDLINE=96394539; PubMed=8798645;
RA Hatada Y., Igarashi K., Ozaki K., Ara K., Hitomi J., Kobayashi T.,
RA "Hatada Y., Igarashi K., Ozaki K., Ara K., Hitomi J., Kobayashi T.;
RT Amylopolylaminase from Bacillus that hydrolyzes alpha-1,4 and alpha-1,6
RT linkages in polysaccharides at different active sites."
RL J. Biol. Chem. 271:24075-24083(1996).
DR EMBL: D78258; BAAL1332.1; -.
DR HSSP: P06278; IVOS.
DR InterPro: IPR000461; -.
DR InterPro: IPR001859; -.
DR Pfam: PF00128; alpha-amylase: 2.
DR Pfam: PF00746; Gram_pos_anchor: 1.
DR PROSITE: PS00133; CARBOXYPEPT_ZN_2; UNKNOWN: 1.
SQ SEQUENCE 1938 AA; 214917 MW; A29D3F715E86A72E CRC64;

Query Match 82.1% Score 32; DB 2; Length 1938;
Best Local Similarity 62.5% Pred. No. 35et02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 SYSSSNV 8
DB 1669 YDSSSNV 1676

RESULT 13
Q19343 PRELIMINARY; PRT; 130 AA.
ID Q19343
AC Q19343;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)

```


THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:12:36 : Search time 77.92 Seconds

(without alignments)
6.224 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSNVV 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Listing files: 45 summaries

Database : A. Geneseq-0601.*

1: /SID8/gcgdata/geneseq/genesep/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/genesep/AA1981.DAT.*
3: /SID8/gcgdata/geneseq/genesep/AA1982.DAT.*
4: /SID8/gcgdata/geneseq/genesep/AA1983.DAT.*
5: /SID8/gcgdata/geneseq/genesep/AA1984.DAT.*
6: /SID8/gcgdata/geneseq/genesep/AA1985.DAT.*
7: /SID8/gcgdata/geneseq/genesep/AA1986.DAT.*
8: /SID8/gcgdata/geneseq/genesep/AA1987.DAT.*
9: /SID8/gcgdata/geneseq/genesep/AA1988.DAT.*
10: /SID8/gcgdata/genesep/genesep/AA1989.DAT.*
11: /SID8/gcgdata/genesep/genesep/AA1990.DAT.*
12: /SID8/gcgdata/genesep/genesep/AA1991.DAT.*
13: /SID8/gcgdata/genesep/genesep/AA1992.DAT.*
14: /SID8/gcgdata/genesep/genesep/AA1993.DAT.*
15: /SID8/gcgdata/genesep/genesep/AA1994.DAT.*
16: /SID8/gcgdata/genesep/genesep/AA1995.DAT.*
17: /SID8/gcgdata/genesep/genesep/AA1996.DAT.*
18: /SID8/gcgdata/genesep/genesep/AA1997.DAT.*
19: /SID8/gcgdata/genesep/genesep/AA1998.DAT.*
20: /SID8/gcgdata/genesep/genesep/AA1999.DAT.*
21: /SID8/gcgdata/genesep/genesep/AA2000.DAT.*
22: /SID8/gcgdata/genesep/genesep/AA2001.DAT.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	8	AA61298	Anti-TANCO 268 scf
2	33	89.7	402	AA60258	Osteogenic Protein
3	33	89.7	713	AA60258	Arbidoopsis thalia
4	33	84.6	752	AA623581	Pulvisense protei
5	32	82.1	798	AAW35552	Bacillus alkaline
6	32	82.1	893	AAW09257	Bacillus alkaline
7	32	82.1	1938	AAW09255	Full length Pulli
8	32	82.1	1938	AAW3553	Subunit of the hum
9	31	79.5	220	AAW2340	Alpha subunit of r
10	31	79.5	220	AAW2340	Polypeptide isolat
11	31	79.5	325	AAW2405	

12	31	79.5	469	AA15510	Tomato ACC synthase
13	31	79.5	964	AAW2619	Cyclic-Isomaltolig
14	30	76.9	129	AAW2106	Peptide 3-49 deriv
15	30	76.9	130	AAW2106	Peptide 3-49 deriv
16	30	76.9	308	AAW4677	Arbidoopsis thalia
17	30	76.9	380	AAW35707	Arbidoopsis thalia
18	30	76.9	390	AAW4676	Arbidoopsis thalia
19	30	76.9	462	AAW35706	Arbidoopsis thalia
20	30	76.9	618	AAW5098	Streptococcus pneu
21	30	76.9	627	AAW1785	Photobacterium Lum
22	30	76.9	627	AAW5344	Toxin CgAb1, encod
23	30	76.9	627	AAW5344	Toxin CgAb1, encod
24	30	76.9	659	AAW8180	Human LFA-1 beta c
25	30	76.9	659	AAW8180	Human LFA-1 beta c
26	30	76.9	769	AAW0835	Beta subunit of hu
27	30	76.9	769	AAW07113	Recombinant beta-s
28	30	76.9	769	AAW24256	Beta-subunit C18
29	30	76.9	769	AAW80108	LFA-1 beta subunit
30	30	76.9	769	AAW03974	LFA-1 CD18 polypep
31	30	76.9	1189	AAW5654	Human CD18 polypep
32	29	74.4	16	AAW33192	Human CD18 polypep
33	29	74.4	40	AAW12037	E. cloacae adhesiv
34	29	74.4	108	AAW82719	Curvularia verticu
35	29	74.4	129	AAW16381	Human antibody lam
36	29	74.4	177	AAW33755	Pinus radiata flav
37	29	74.4	246	AAW03434	Enuatiptus grandis
38	29	74.4	257	AAW03434	Anti CD19 antibody
39	29	74.4	281	AAW82314	Human SCpVD19 to
40	29	74.4	285	AAW14200	Mouse DNK demethyl
41	29	74.4	288	AAW82316	Mouse OX73 variant
42	29	74.4	288	AAW82317	Mouse DNK demethyl
43	29	74.4	291	AAW41198	Human B1 demethyl
44	29	74.4	469	AAW59726	Tomato ACC synthase
45	29	74.4	483	AAW82315	Chimeric CD19/CTCR

ALIGNMENTS

RESULT 1	AA61298	standard: Peptide: 8 AA.
AA61298:		
04-APR-2001 (first entry)		
DE	Anti-TANCO 268 scfV CDR, SEQ ID NO: 66.	
XX	Human: antibody: scfV: CDR: complementarity determining region:	
XX	TANCO 268: caridant: cerebroprotective: cytotoxic: anticonvulant:	
XX	thrombolytic: antiarteriosclerotic: haemostatic: glycoprotein VI: GPVI:	
KW	platelet membrane glycoprotein receptor: bleeding disorder:	
KW	ischemia: injury: thrombotic disorder: haemorrhagic disorder: stroke:	
KW	ischemia: cardiovascular disease: immunological disease: liver disorder:	
KW	cancer:	
XX		
XX	homo sapiens.	
XX		
XX	MO200100810-A1.	
XX		
PD	04-JAN-2001.	
XX	30-JUN-2000: 2000MO-US81512.	
XX	AAW2340: 2000MO-US81512.	
XX	30-JUN-1999: 99US-045468.	
PR	06-DEC-1999: 99US-0454824.	
XX	14-FEB-2000: 2000US-050387.	
PR		
XX	(MILL.) MILLENNIUM PHARM INC.	
XX		
XX	Bufield SJ, Wallerai J, Jandrot-Perrus M, Valenchenker W, Gill DS,	
PI	Qian MO, Kingsbury G.	

XX WPI: 2001-080877/09.
 PT New genes encoding human platelet-expressed collagen receptor.
 PT glycoprotein VI and the alpha2beta1 integrin, involved in preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders -
 XX
 XX Claim 32: Page 102: 227pp: English.
 XX
 XX The present sequence is given in a specification relating to an isolated
 XX nucleic acid and to a recombinant expression vector encoding the glycoprotein receptor
 XX glycoprotein VI (GPVI) also called RMO2 268
 XX and polypeptides and their modulators, e.g. antisense nucleic acids,
 XX ribozymes and antibodies, are useful for preventing, treating and
 XX diagnosing disorders associated with aberrant expression or activity of
 XX GPVI. These disorders include bleeding disorders
 XX (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
 XX (e.g. coronary occlusion of the coronary arteries), hemorrhagic
 XX disorders, coronary artery diseases (e.g. stroke and
 XX ischemia), cardiovascular diseases (e.g. atherosclerosis, myocardial
 XX infarction), immunological diseases (e.g. platelet disorder) and
 XX embryonic liver disorders. Preferably they are used to prevent acute
 XX cardiac ischemia following angioplasty and metastatic cancers,
 XX especially of the colon and liver.
 XX
 XX Sequence 8 AA:
 SQ

Query Match 100.0%; Score 39; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYSSSNV 8
 |||||||
 DB 1 sydsnsv 8

RESULT 2

AA060578
 AA060578 standard; Protein; 402 AA.

AA060578:

30-MAR-1995 (first entry)

Osteogenic protein OP2.

Osteogenic protein.

Homo sapiens.

Key Location/Qualifiers

Cleavage-site 239..242 /note= "proteolytic cleavage site"

Cleavage-site 260..263 /note= "proteolytic cleavage site"

MO9420539-A.

15-SEP-1994.

04-MAR-1994: 94MO-0502335.

04-MAR-1993: 93US-0027070.

(CERA-) CREATIVE BIOMOLECULES INC.

Jones MR, Oppermann H, Ozkaynak E, Rueger DC, Sampath KT;

Tucker RF;

WPI: 1994-302971/37.

N-PDB; A0071406.

XX Binding partners, esp. antibodies, specific for different forms
 PT of osteogenic protein - for differentiating between mature and
 PT soluble complexed forms of the protein in culture media or serum.
 XX
 XX Disclosure: Page 50-52: 70pp: English.
 XX
 XX The osteogenic protein is produced recombinantly in mammalian cell
 XX cultures, and may be provided to a site for bone induction in a
 XX mammal with a suitable matrix to allow infiltration, proliferation
 XX and differentiation of migrating progenitor cells.
 XX
 XX Sequence 402 AA:
 SQ

Query Match 89.7%; Score 35; DB 15; Length 402;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YDSSSNV 8
 |||||||
 DB 380 ydsnsv 386

RESULT 3

AA029582
 AA029582 standard; Protein; 730 AA.

AA029582:

17-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 35222.

Protein identification, signal transduction pathway; metabolic pathway;

Protein identification; genetic mapping; gene expression control; promoter;

Arabidopsis thaliana.

EP103405-A2.

06-SEP-2000.

25-FEB-2000: 2000EP-0301439.

25-FEB-1999: 99US-0121825.

05-MAR-1999: 99US-0123180.

05-MAR-1999: 99US-0123548.

25-MAR-1999: 99US-0125788.

25-MAR-1999: 99US-0126784.

25-MAR-1999: 99US-0126784.

01-APR-1999: 99US-0127462.

06-APR-1999: 99US-0128234.

08-APR-1999: 99US-0128714.

16-APR-1999: 99US-0129845.

15-APR-1999: 99US-0130077.

21-APR-1999: 99US-0130445.

21-APR-1999: 99US-0130445.

21-APR-1999: 99US-0130891.

28-APR-1999: 99US-0131449.

30-APR-1999: 99US-0132048.

30-APR-1999: 99US-0132407.

04-MAY-1999: 99US-0132485.

05-MAY-1999: 99US-0132485.

06-MAY-1999: 99US-0132485.

07-MAY-1999: 99US-0132487.

11-MAY-1999: 99US-0134256.

14-MAY-1999: 99US-0134216.

14-MAY-1999: 99US-0134219.

14-MAY-1999: 99US-0134221.

14-MAY-1999: 99US-0134370.

PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134541.
PR 20-MAY-1999; 99US-0132324.
PR 21-MAY-1999; 99US-0135629.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137722.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 16-JUN-1999; 99US-0139454.
PR 16-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139859.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141882.
PR 02-JUL-1999; 99US-0142054.
PR 06-JUL-1999; 99US-0142300.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0143631.
PR 16-JUL-1999; 99US-0144082.
PR 16-JUL-1999; 99US-0144086.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144684.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145216.
PR 26-JUL-1999; 99US-0145216.
PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145519.
PR 28-JUL-1999; 99US-0145521.
PR 28-JUL-1999; 99US-0145521.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147392.
PR 06-AUG-1999; 99US-0147393.
PR 06-AUG-1999; 99US-0147393.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148317.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149375.
PR 18-AUG-1999; 99US-0149375.
PR 20-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149725.
PR 21-AUG-1999; 99US-0149729.
PR 21-AUG-1999; 99US-0149910.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151418.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152383.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153798.
PR 13-SEP-1999; 99US-0153798.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154719.
PR 22-SEP-1999; 99US-0155119.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157163.
PR 05-OCT-1999; 99US-0157163.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158292.
PR 12-OCT-1999; 99US-0158393.
PR 12-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159310.
PR 14-OCT-1999; 99US-0159310.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160748.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160950.
PR 22-OCT-1999; 99US-0160951.
PR 22-OCT-1999; 99US-0160959.
PR 22-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.

PR	14-OCT-1993	9905.0147702	PR	14-OCT-1993	9905.0147702
PR	05-AUG-1999	9905.0147702	PR	05-AUG-1999	9905.0147702
PR	05-AUG-1999	9905.0147760	PR	05-AUG-1999	9905.0147760
PR	06-AUG-1999	9905.0147760	PR	06-AUG-1999	9905.0147760
PR	05-AUG-1999	9905.0147835	PR	05-AUG-1999	9905.0147835
PR	09-AUG-1999	9905.0147935	PR	09-AUG-1999	9905.0147935
PR	11-AUG-1999	9905.0148171	PR	11-AUG-1999	9905.0148171
PR	12-AUG-1999	9905.0148341	PR	12-AUG-1999	9905.0148341
PR	13-AUG-1999	9905.0148545	PR	13-AUG-1999	9905.0148545
PR	17-AUG-1999	9905.0148758	PR	17-AUG-1999	9905.0148758
PR	18-AUG-1999	9905.0149126	PR	18-AUG-1999	9905.0149126
PR	20-AUG-1999	9905.0149226	PR	20-AUG-1999	9905.0149226
PR	20-AUG-1999	9905.0149723	PR	20-AUG-1999	9905.0149723
PR	23-AUG-1999	9905.0149902	PR	23-AUG-1999	9905.0149902
PR	23-AUG-1999	9905.0149930	PR	23-AUG-1999	9905.0149930
PR	25-AUG-1999	9905.0150084	PR	25-AUG-1999	9905.0150084
PR	27-AUG-1999	9905.0150865	PR	27-AUG-1999	9905.0150865
PR	27-AUG-1999	9905.0151060	PR	27-AUG-1999	9905.0151060
PR	30-AUG-1999	9905.0151303	PR	30-AUG-1999	9905.0151303
PR	31-AUG-1999	9905.0151438	PR	31-AUG-1999	9905.0151438
PR	07-SEP-1999	9905.0152240	PR	07-SEP-1999	9905.0152240
PR	10-SEP-1999	9905.0153070	PR	10-SEP-1999	9905.0153070
PR	13-SEP-1999	9905.0153758	PR	13-SEP-1999	9905.0153758
PR	15-SEP-1999	9905.0154018	PR	15-SEP-1999	9905.0154018
PR	16-SEP-1999	9905.0154479	PR	16-SEP-1999	9905.0154479
PR	22-SEP-1999	9905.0155139	PR	22-SEP-1999	9905.0155139
PR	22-SEP-1999	9905.0155589	PR	22-SEP-1999	9905.0155589
PR	23-SEP-1999	9905.0155656	PR	23-SEP-1999	9905.0155656
PR	28-SEP-1999	9905.0156594	PR	28-SEP-1999	9905.0156594
PR	04-OCT-1999	9905.0157117	PR	04-OCT-1999	9905.0157117
PR	05-OCT-1999	9905.0157753	PR	05-OCT-1999	9905.0157753
PR	06-OCT-1999	9905.0157865	PR	06-OCT-1999	9905.0157865
PR	07-OCT-1999	9905.0158029	PR	07-OCT-1999	9905.0158029
PR	08-OCT-1999	9905.0158232	PR	08-OCT-1999	9905.0158232
PR	11-OCT-1999	9905.0158283	PR	11-OCT-1999	9905.0158283
PR	13-OCT-1999	9905.0159224	PR	13-OCT-1999	9905.0159224
PR	14-OCT-1999	9905.0159330	PR	14-OCT-1999	9905.0159330
PR	14-OCT-1999	9905.0159537	PR	14-OCT-1999	9905.0159537
PR	14-OCT-1999	9905.0159531	PR	14-OCT-1999	9905.0159531
PR	14-OCT-1999	9905.0159577	PR	14-OCT-1999	9905.0159577
PR	16-OCT-1999	9905.0159588	PR	16-OCT-1999	9905.0159588
PR	21-OCT-1999	9905.0160741	PR	21-OCT-1999	9905.0160741
PR	21-OCT-1999	9905.0160768	PR	21-OCT-1999	9905.0160768
PR	21-OCT-1999	9905.0160770	PR	21-OCT-1999	9905.0160770
PR	21-OCT-1999	9905.0160814	PR	21-OCT-1999	9905.0160814
PR	21-OCT-1999	9905.0160815	PR	21-OCT-1999	9905.0160815
PR	22-OCT-1999	9905.0160981	PR	22-OCT-1999	9905.0160981
PR	22-OCT-1999	9905.0161040	PR	22-OCT-1999	9905.0161040
PR	25-OCT-1999	9905.0161406	PR	25-OCT-1999	9905.0161406
PR	26-OCT-1999	9905.0161539	PR	26-OCT-1999	9905.0161539
PR	26-OCT-1999	9905.0161561	PR	26-OCT-1999	9905.0161561
PR	28-OCT-1999	9905.0161920	PR	28-OCT-1999	

```

Query Match Score 84.6%; Score 33; DB 21; Length 752;
Best Local Similarity 71.4%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

QY      2 YDSNNV 8
Db      533 ydsnll 539

RESULT      5
AC          AA073552
AC          AA073552 standard; protein: 798 AA.
AC          AA073552:
AC          08-MAR-1999 (first entry)
AC          Pullulanase protein.
AC          Pullulanase; variant; bleach-containing detergent; oxidation resistant.
OS          Bacillus sp.
OS          JP10327868-A.
PD          15-DEC-1998.
PF          30-MAY-1997; 97JP-0141596.
PR          30-MAY-1997; 97JP-0141596.
PR          (KAOS ) KAO CORP.
PR          WPI; 1999-099031/09.
PT          New mutant pullulanase - useful in bleach-containing detergents
PT          Claim 11; Page 8-10; 19pp; Japanese.
PS          xx
PS          xx
PS          Claim 11; Page 8-10; 19pp; Japanese.
CC          This sequence represents the Bacillus pullulanase protein. The 479yeilon
CC          residue at the 14th position is a glutamic acid. The 14th residue in the
CC          residue at the 14th position is a glutamic acid. The 14th residue in the
CC          residue other than Cys and Met and/or at least one alanine residue in the
CC          amino acid residues constituting pullulanase is deleted or replaced by an
CC          optional amino acid residue other than Ala. The mutant pullulanase is
CC          useful in bleach-containing detergents. The pullulanase is highly
CC          resistant to oxidation.
CC          xx
CC          xx
CC          Sequence 798 AA:
QY      Query Match      82.1%; Score 32; DB 20; Length 798;
QY      Best Local Similarity 62.5%; Pred. No. 1,4e+02;
QY      Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      1 YDSNNV 8
QY      |||||:
Db      647 ydsnll 654

RESULT      6
AC          AA009257
AC          AA009257 standard; Protein: 893 AA.
AC          AA009257:
AC          27-MAR-1997 (first entry)
AC          D
AC          Bacillus alkaline pullulanase.
AC          xx
AC          xx
AC          Anylopullulanase; alpha-amylase; pullulanase; detergent additive.
AC          xx

```

OS	Bacillus sp. KSM-AP1378 (EEM BP-3048).
XX	
XX	Key
XX	Peptide
XX	1..32
XX	/label=Sig.peptide
XX	33..1938
XX	/label=Mat.protein
XX	1906..813
XX	/label=Immature amy[opu]lulanase*
XX	328..813
XX	/label=Immature amy[opu]lulanase
XX	/note="N-terminal alpha-amylose"
XX	462..645
XX	/note="amylose active centre"
XX	462..467
XX	/label=Region-I
XX	546..554
XX	/label=Region-II
XX	/note="amylose active centre region II"
XX	579..582
XX	/label=Region-III
XX	/note="amylose active centre region III"
XX	640..645
XX	/label=Region-IV
XX	/note="amylose active centre region IV"
XX	834..866
XX	/note="Intervening sequence"
XX	944..976
XX	/note="Intervening sequence"
XX	1046..1938
XX	/label=Pullulanase
XX	/note="N-terminal alkaline pullulanase"
XX	/note="pullulanase active centre"
XX	1396..1401
XX	/label=Region-I
XX	/note="pullulanase active centre region I"
XX	1460..1468
XX	/label=Region-II
XX	/note="pullulanase active centre region II"
XX	1503..1509
XX	/label=Region-III
XX	/note="pullulanase active centre region III"
XX	1576..1581
XX	/label=Region-IV
XX	/note="pullulanase active centre region IV"
XX	
XX	MO9635794-A1.
XX	
XX	14-NOV-1996.
XX	
XX	10-MAY-1996.
XX	96MO-JP01243.
XX	
XX	10-MAY-1995.
XX	95JP-0111547.
XX	
XX	(KAOS) KAO CORP.
XX	
XX	ARA K, Hatada Y, Igarashi K, Ito S, Kawai S, Ozaki K.
XX	WPI: 1996-518682/51.
XX	N-PSDB: AAT47878.
XX	
XX	DNA encoding alkaline pullulanase having alkaline alpha-amylose
XX	activity - useful for improving the efficiency of dish washing
XX	degreasers and detergents for clothes, esp. on starch soils
XX	
XX	Disclosure: Page 42-54: 75pp: English.
XX	
XX	Anylopullulanase (AA090255) of Bacillus sp. isolate KSM-AP1378 has an
XX	N-terminal alkaline alpha-amylose moiety (see also AA090256) and a
XX	C-terminal alkaline pullulanase moiety (see also AA090257). It is
XX	the product of an open reading frame in a DNA fragment (AAT47878)

CC anti(pullulanase, alpha-amylase and pullulanase can each be
 CC expressed in transformed host cells using the appropriate
 CC appropriate gene fragments. The enzymes are useful as additives
 CC in dish-washing and clothes detergent compans.

XX Sequence 1938 AA;

Query Match 82.1%; Score 32; DB 17; Length 1938;
 Best Local Similarity 62.5%; Tree NC 3; e=0.0;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SYSSSNV 8
 Db 1669 sysditi 1676

RESULT 8
 AAW73553
 ID AAW73553 standard; protein: 1938 AA.

XX AAW73553;
 AC
 XX
 XX 08-MAR-1999 (first entry)
 DT
 XX
 XX Full length Pullulanase protein.

XX Pullulanase; variant: bleach-containing detergent; oxidation resistant.

XX Bacillus sp.

XX Key Location/Qualifiers
 XX MISC-difference 123..119 "nucleotides encoding these residues are not
 FT present in the coding sequence given in the
 FT "specification"
 FT MISC-difference 1050..1065
 FT "note=" "nucleotides encoding these residues are not
 FT present in the coding sequence given in the
 FT "specification"

XX JP10327868-A.

XX 15-DEC-1998.

XX 30-MAY-1997; 97JP-0141596.

XX 30-MAY-1997; 97JP-0141596.

XX (KAOS) KAO CORP.

XX WPI: 1999-099031/09.

XX N-PSDB; AAW62881.

XX New mutant pullulanase - useful in bleach-containing detergents

XX Claim 13; Page 10-17; 19pp; Japanese.

XX This sequence represents the Bacillus pullulanase protein. The invention
 CC relates to a mutant pullulanase in which at least one methionine residue
 CC in the pullulanase is deleted or replaced by an optional amino acid
 CC residue other than Cys and Met and/or at least one alanine residue in the
 CC amino acid residues constituting pullulanase is deleted or replaced by an
 CC amino acid residue other than Cys and Met and/or at least one alanine residue
 CC is useful in bleach-containing detergents. The pullulanase is highly
 CC resistant to oxidation.

XX Sequence 1938 AA;

Query Match 82.1%; Score 32; DB 20; Length 1938;
 Best Local Similarity 62.5%; Tree NC 3; e=0.0;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYSSSNV 8
 Db 1669 sysditi 1676

RESULT 9
 AAW42340
 ID AAW42340 standard; Protein: 220 AA.

XX AAW42340;

XX 21-JUN-1994 (first entry)

XX Subunit of the human IgE receptor.

XX IgE; immunoglobulin E receptor; beta subunit; basophil; allergy;
 XX 899-0401; signal transduction; diagnosis; antagonist.

XX Homo sapiens.

XX MO9321317-A.

XX 28-OCT-1993.

XX 16-APR-1993; 93NO-US03419.

XX 16-APR-1993; 92US-0869933.

XX (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX Kinect JP.

XX WPI: 1993-35127/44.

XX Immunoglobulin E receptor human beta sub-unit isolation - using
 PT 1st strand reverse transcripts from human basophils as templates
 PT for a polymerase chain reaction, used to treat and diagnose
 PT allergic diseases

XX Disclosure: Fig 12; 154pp; English.

XX The sequence is that of a subunit of the human IgE receptor.
 CC The protein can be used to identify human beta subunit
 CC FcεRI inhibitors (immunoglobulin E receptor) which inhibit the
 CC binding of IgE to its receptor and inhibit the aggregation function
 CC of the receptor or the signal transducing function related to
 CC allergic response. Such inhibitors can be used for the treatment or
 CC prevention of allergic disease.
 CC See also AAW4237-42.

XX Sequence 220 AA;

Query Match 79.5%; Score 31; DB 14; Length 220;
 Best Local Similarity 72.4%; Tree NC 5;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYSSNV 7
 Db 130 sysditi 136

RESULT 10
 AAW90386
 ID AAW90386 standard; protein: 245 AA.

XX AAW90386;

XX 01-NOV-1989 (first entry)

XX Alpha subunit of rat mast cell IgE surface receptor.

KW Immunoglobulin E receptor alpha subunit:
 KW allergies; non-peptide drug design; rat.
 XX Rat.
 CC MO8905352-A.
 CC
 XX
 PD 15-JUN-1989.
 CC
 XX
 PF 29-NOV-1988: 88MO-US04255.
 XX
 PK 01-DEC-1987: 87US-0127214.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strigamian R, Shinku A, Leder P, Bentley P;
 DR WPI: 1989-192698/26.
 DR N-PSDB: AAN90125.
 XX
 PT cDNA encoding IgE receptor alpha-subunit - used to treat allergies.
 PS
 XX Disclosure: fig 4; 17pp; English.
 PS
 CC Immunoglobulin E receptor alpha subunit of rat mast cell IgE
 CC surface receptor (see corresp. AAN90125) . Used to produce antibodies
 CC to the receptor (see corresp. AAN90125) . Used to produce antibodies
 CC and design non-peptide drugs.
 CC
 XX Sequence 245 AA:
 SQ

Query Match 79.5%; Score 31; DB 10; Length 245;
 Best Local Similarity 71.4%; Pred. No. 57;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYSDSNV 7
 DB 153 sysdm1 159

RESULT 11
 ID AAY02465
 XX AAY02465 standard; protein: 325 AA.
 AC AAY02465;
 XX
 DT 13-JUL-1999 (first entry)
 XX
 DR Polypeptide isolated from prostate tissue.
 XX
 KW N-terminal; prostate tumour cell; immunogenic; treatment; diagnosis;
 KW Prostate cancer.
 XX
 OS Homo sapiens.
 XX
 CC MO9518210-A2.
 CC
 PD 15-APR-1999.
 CC
 PF 07-OCT-1998: 98MO-US21166.
 XX
 PR 23-JUN-1998: 98US-0102679.
 PR 07-OCT-1997: 97US-0946026.
 XX
 PK (CORI-) CORIAX CORP.
 XX
 PI Dillon DC, Mitchem JL, Reed SG, Twardzik DR;
 DR WPI: 1999-277272/23.
 DR
 XX New isolated prostate polypeptides useful for the treatment,
 PT diagnosis and monitoring of prostate cancer.
 PT

XX
 PS Example 6: Page 93-94; 106pp; English.
 XX
 CC The present sequence represents a polypeptide obtained from prostate
 CC tumour cells. The polypeptide comprises an immunogenic portion of a
 CC prostate protein. The polypeptides and DNA obtained from prostate
 CC tumour cells (see corresp. AAN90125) are disclosed as diagnostic tools
 CC be used in the treatment, diagnosis and monitoring of prostate cancer.
 XX
 SQ Sequence 325 AA:

Query Match 79.5%; Score 31; DB 20; Length 325;
 Best Local Similarity 65.7%; Pred. No. 79;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYSDSNV 7
 DB 97 sysdm1 103

RESULT 12
 ID AAR15510
 XX AAR15510 standard; Protein: 469 AA.
 AC AAR15510;
 XX
 DT 09-MAR-1992 (first entry)
 XX
 DR Tomato ACC synthase encoded by clone LE-ACC3.
 XX
 KW 1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening.
 XX
 CC Lycopersicon esculentum c.v. Rutgers.
 CC
 OS US7579896-A.
 XX
 PD 12-NOV-1991.
 XX
 PF 10-SEP-1990: 90US-0579896.
 XX
 PR 10-SEP-1990: 90US-0579896.
 XX
 PK (USDA) US SPEC OF AGRICULTURE.
 XX
 PI Theologas A, Sato T;
 DR WPI: 1991-368895/50.
 XX
 DR DNA encoding ACC synthase - used for control of plant development
 PT and for prodn. of ACC synthase, ethylene and ethanol
 PT
 PS Disclosure: Fig 14; 73pp; English.
 XX
 CC Genomic clone LE-ACC1A was one of four different clones identified
 CC in a library prepared from total DNA extracted from etiolated Rutgers
 CC seedlings. Screening was by the cDNA clone pACC1 (see AAO15134). The
 CC amino acid sequence was deduced from the cDNA and shows
 CC considerable homology with ACC sequences deduced from the three other
 CC sequences of tomato ACC synthase clones.
 CC See AAO15131-Q15140.
 XX
 SQ Sequence 469 AA:

Query Match 79.5%; Score 31; DB 12; Length 469;
 Best Local Similarity 62.3%; Pred. No. 1,26702;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYSDSNV 8
 DB 108 sysdm1 115

```

RESULT 13
AAW22619
ID AAW22619 standard; Protein: 964 AA.
XX
AC AAW22619;
XX
XX 04-FEB-1998 (first entry)
XX
DE Cyclic-Isomaltoligosaccharide synthase.
XX
XX Cyclic-Isomaltoligosaccharide synthase; cyclotransomaltotriose;
XX anti-decay activity; Escherichia coli; E.coli; microorganism;
XX recombinant DNA.
XX
XX Bacillus sp.
XX
XX JF09234073-A.
XX
XX 09-SEP-1997.
XX
XX
XX 01-MAR-1996; 96JP-0045103.
XX
XX 01-MAR-1996; 96JP-0045103.
XX
XX (MORO ) NORINSUISANSIO SHOKUJIN SOCO.
XX (MORA ) ZH NODA SANGYO KAGAKU KENKYUSHO.
XX
XX NPI; 1997-497314/46.
XX
XX N-PSDB; AAT92376.
XX
XX Cyclic-Isomaltoligosaccharide synthase - used in the production of
XX cyclo-Isomaltotriose with strong anti-decay activity
XX
XX Claim 3: Page 8-10; 12pp; Japanese.
XX
XX
XX The present sequence represents a novel cyclic-Isomaltoligosaccharide
XX synthase isolated from a Bacillus sp. (possibly Bacillus circulans
XX syn311). The cyclic-Isomaltoligosaccharide synthase has the following
XX physical properties: molecular weight of 100,000; pI of 4.5; and
XX dextran) consisting of 1,6-alpha-linkages to form cyclic
XX Isomaltoligosaccharides based on cyclotransomaltotriose; (2) substrate
XX specificity: acts on dextran having 1,6-alpha-linkages as main chains,
XX but not on amylopectin, pullulan; and (3) optimum pH and stable pH
XX range: active around pH 6.0 and produce in the range of pH 4.5 to 9.0.
XX The DNA sequence may be used to produce cyclic-Isomaltoligosaccharide
XX synthase in microorganisms of the genus Escherichia, particularly
XX E.coli. The results indicate that the cyclic-Isomaltoligosaccharide
XX synthase can efficiently produce cyclotransomaltotriose which has very strong
XX anti-decay activity.
XX
XX
XX Sequence 964 AA:
XX
XX
XX Query Match 76.5%; Score 31; DA 18; Length 964;
XX Best Local Similarity 100.0%; Pred No 2; Re102;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SYDSNN 6
XX I I I I I I I
XX DB 521 sydsnn 526
XX
XX
XX RESULT 14
XX AAR22106
XX ID AAR22106 standard; Protein: 29 AA.
XX
XX AAR22106;
XX
XX 15-JUL-1992 (first entry)
XX
XX Peptide 3-29 derived from CD18 Leukocyte Integrin.
XX

```

```

XX
XX Cell adhesion; intercellular adhesion molecule; endothelium;
XX inflammation; leukocyte chemotaxis; rhinovirus; common cold.
XX
XX W09203473-A.
XX
XX
XX 05-MAR-1992.
XX
XX 23-AUG-1991; 91WO-0006063.
XX
XX 27-AUG-1990; 90US-0573624.
XX
XX (CETU ) CETUS CORP.
XX
XX Liu DY, Kaymakcalan Z, Mundy K;
XX
XX WPI; 1992-096833/12.
XX
XX
XX Peptide(s) derived from beta sub-unit CD18 of leukocyte integrins
XX - prevent leukocyte binding to ICAM and leukocyte chemotaxis, for
XX treating inflammatory diseases and rhinoviral infection
XX
XX Claim 2: Page 23; 31pp; English.
XX
XX
XX This peptide (derived from CD18 - see AAR22106) was synthesised and
XX tested for capacity to interfere with or block adhesion of
XX rhinovirus to cells expressing CD18. The peptide shows inhibitory
XX activity against rhinovirus infection. The peptide can be used to
XX treat/prevent inflammation and can inhibit binding
XX of viruses to endothelium. See AAO22780 and AAR22104-R22112.
XX
XX
XX Sequence 29 AA:
XX
XX
XX Query Match 76.9%; Score 30; DA 13; Length 29;
XX Best Local Similarity 87.5%; Pred No 8; I;
XX Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 SYDSNNV 8
XX I I I I I I I I
XX DB 10 sedsnv 17
XX
XX
XX RESULT 15
XX AAW64528
XX ID AAW64528 standard; Protein: 126 AA.
XX
XX AAW64528;
XX
XX 18-NOV-1998 (first entry)
XX
XX
XX Papillomavirus major capsid protein L1 from plasmid DL369.
XX
XX Major capsid protein L1; epithelial neoplasm; diagnosis; infection;
XX therapy; vaccine.
XX
XX human papillomavirus.
XX
XX Key Location/Qualifiers
XX FT Protein 1..126 /note="partial sequence"
XX
XX DE19735118-Cl.
XX
XX 13-AUG-1998.
XX
XX 13-AUG-1997; 97DE-1035118.
XX
XX 13-AUG-1997; 97DE-1035118.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX De Villiers zur Hausen E, zur Hausen H;
XX

```

DR WPI: 1998-415283/36.
 DR N-PSDB: AAV45545.
 XX
 XX
 XX
 XX
 XX
 PS Papilloma virus DNA - coding for major capsid protein
 PS Claim 1; Fig 3; 12pp; German.
 XX
 CC This sequence represents a human papillomavirus major capsid protein L1
 CC which has been isolated from plasmid pL369 using total DNA from an
 CC epithelial neoplasm biopsy. Transformants can be cultured to produce
 CC the protein. The DNA can be used as a reagent for diagnosis of papilloma
 CC virus infections. The protein can be used for diagnosis or therapy of
 CC papilloma virus infections or for vaccination against such infections.
 XX
 SO Sequence 126 AA;

Query Match 76.98; Score 30; DB 19; Length 126;
 Best Local Similarity 83.3%; Pred. No. 44;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YDSSNV 7
 |||||
 Db 30 ydsam1 35

Search completed: November 19, 2001, 08:12:37
 Job time: 90 sec

GenCode version 4.5
Copyright (c) 1993 - 2000 Compaq Inc.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:23:16 : Search time 526.89 Seconds
(without alignments)
4,216 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 STYSSNV 8

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 3148936 segs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents, AA, Main :
1: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
2: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
3: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
4: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
5: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
6: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
7: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
8: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
9: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
10: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
11: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
12: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
13: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
14: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
15: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
16: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
17: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
18: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
19: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
20: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
21: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
22: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
23: /cgn2_6/pdata/2/paa/US081.COMB.pep.*
24: /cgn2_6/pdata/2/paa/US081.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	8	1 PCT-US00-18152-66	Sequence 66, Appl
2	39	100.0	8	20 US-09-610-118-66	Sequence 66, Appl
3	39	100.0	8	22 US-09-610-118-66	Sequence 66, Appl
4	39	100.0	8	22 US-09-610-118-66	Sequence 66, Appl
5	39	100.0	8	22 US-09-610-118-66	Sequence 66, Appl
6	39	100.0	8	22 US-09-610-118-66	Sequence 66, Appl
7	39	100.0	8	22 US-09-610-118-66	Sequence 66, Appl
8	39	100.0	8	22 US-09-610-118-66	Sequence 66, Appl
9	39	100.0	8	22 US-09-610-118-66	Sequence 66, Appl

10	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
11	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
12	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
13	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
14	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
15	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
16	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
17	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
18	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
19	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
20	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
21	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
22	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
23	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
24	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
25	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
26	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
27	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
28	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
29	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
30	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
31	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
32	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
33	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
34	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
35	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
36	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
37	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
38	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
39	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
40	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
41	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
42	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
43	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
44	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap
45	32	82.1	515	15	US-09-107-532-5317	Sequence 5317, Ap

ALIGNMENTS

Result 1
Sequence 66, Application PCT/US0018152
GENERAL INFORMATION:
TITLE OF INVENTION: GLYCOPROTEIN VI AND USGS THERMOF
FILE REFERENCE: 7853-211-228 PCT/US00/018152
CURRENT APPLICATION NUMBER: PCT/US00/018152
EARLIER APPLICATION NUMBER: 09/503,387
EARLIER FILING DATE: 2/14/00
EARLIER APPLICATION NUMBER: 09/454,824
EARLIER FILING DATE: 12/6/99
EARLIER APPLICATION NUMBER: 09/345,468
EARLIER FILING DATE: 6/20/99
INVENTOR: JAMES H. WILSON, JR.
SOFTWARE: PARSED FOR Windows Version 3.0
SEQ ID NO 66
LENGTH: 8
TYPE: PPT
ORGANISM: Homo sapiens
PCT-US00-18152-66

Query Match 100.0%: Score 39, DB 1: Length 8;
Best Local Similarity 100.0%: Pred. No. 2,9e+06;
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
OY 1 STYSSNV 8
DB 1 STYSSNV 8


```

? APPLICANT: Li, Peter M.D.
? TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS
? TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
? FILE REFERENCE: C1000173
? CURRENT APPLICATION NUMBER: US/60/173,464
? CURRENT FILING DATE: 1999-12-29
? NUMBER OF SEQ ID NOS: 30269
? SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
? SEQ ID NO 10568
? LENGTH: 1945
? TYPE: PRT
? ORGANISM: Drosophila
US-60-173-464-19058

```

```

Query Match
Best Local Similarity 84.6%; Score 33; DB 24; Length 1945;
Pct Ident 62.5%; Pct Ident 2.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SYSSSNV 8
DB 1266 SYSSSNIT 1273

```

```

RESULT 7
US-60-191-637-23222
? Sequence 23222, Application US/60191637
? GENERAL INFORMATION:
? APPLICANT: Venter, J. Craig
? TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
? TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
? FILE REFERENCE: C1000392
? CURRENT APPLICATION NUMBER: US/60/191,637
? CURRENT FILING DATE: 2000-03-23
? NUMBER OF SEQ ID NOS: 42660
? SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
? SEQ ID NO 23222
? TYPE: PRT
? ORGANISM: DROSOPHILA
US-60-191-637-23222

```

```

Query Match
Best Local Similarity 84.6%; Score 33; DB 24; Length 1945;
Pct Ident 62.5%; Pct Ident 2.7e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SYSSSNV 8
DB 1266 SYSSSNIT 1273

```

```

RESULT 8
US-60-191-681-18308
? Sequence 18308, Application US/60191681
? GENERAL INFORMATION:
? APPLICANT: Li, Peter, M.D.
? TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
? TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
? FILE REFERENCE: C1000392
? CURRENT APPLICATION NUMBER: US/60/191,661
? CURRENT FILING DATE: 2000-03-23
? NUMBER OF SEQ ID NOS: 30973
? SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
? SEQ ID NO 18308
? LENGTH: 1945
? TYPE: PRT
? ORGANISM: DROSOPHILA
US-60-191-681-18308

```

```

QY 1 SYSSSNV 8
DB 1266 SYSSSNIT 1273

```

```

RESULT 9
US-09-270-767-32375
? Sequence 32375, Application US/09270767
? GENERAL INFORMATION:
? APPLICANT: Homburger et al.
? TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
? FILE REFERENCE: File Reference: 7326-094
? CURRENT FILING DATE: 1995-03-17
? NUMBER OF SEQ ID NOS: 62517
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 32375
? LENGTH: 96
? TYPE: PRT
? ORGANISM: Drosophila melanogaster
US-09-270-767-32375

```

```

Query Match
Best Local Similarity 82.1%; Score 32; DB 16; Length 96;
Pct Ident 62.5%; Pct Ident 1.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SYSSSNV 8
DB 85 SYDANIV 92

```

```

RESULT 10
US-09-107-532-5317
? Sequence 5317, Application US/09107532
? GENERAL INFORMATION:
? APPLICANT: Doucette-Stamm and David Bush
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
? TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR
? NUMBER OF SEQUENCES: 7308
? CORRESPONDENCE ADDRESS:
? ADDRESS: GENE THERAPEUTICS CORPORATION
? CITY: Wellesley
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02154
? COMPUTER READABLE FORM:
? MEDIUM TYPE: CD-ROM ISO9660
? SOFTWARE:
? CURRENT APPLICATION DATA:
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/ 085598
? FILING DATE: May 14, 1996
? PRIORITY DATA:
? APPLICATION NUMBER: 60/051571
? FILING DATE: July 2, 1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Atinelleio, Pamela Denike
? REGISTRATION NUMBER: 40,489
? REFERENCE/DOCKET NUMBER: GTC-012
? TELEPHONE: (781)853-5007

```

TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 5317:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 515 amino acids
 TYPE: amino acid
 MOTIF: C-terminal
 MOTIF TYPE: protein
 HYPOTHEICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1...515
 US-09-107-532-5317

Query Match 82.1%; Score 32; DB 15; Length 515;
 Best Local Similarity 85.7%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYSSSNV 7
 Db 175 AADSSNV 181

RESULT 11
 US-09-107-532A-5317
 Sequence 5317, Application US/09107532A
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 CITY: Wallingford
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02354

COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 OPERATING SYSTEM: <unknown>
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 APPLICATION DATE: 10-May-1998
 FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Attinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-8277
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5317:

SEQUENCE CHARACTERISTICS:
 LENGTH: 515 amino acids
 TYPE: amino acid
 MOTIF: C-terminal
 MOTIF TYPE: protein
 HYPOTHEICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (b) LOCATION 1...515
 SEQUENCE DESCRIPTION: SEQ ID NO: 5317:

US-09-107-532A-5317

Query Match 82.1%; Score 32; DB 15; Length 515;
 Best Local Similarity 85.7%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYSSSNV 7
 Db 175 AADSSNV 181

RESULT 12
 US-60-187-217-9945
 Sequence 9945, Application US/60187217
 GENERAL INFORMATION:
 APPLICANT: Li, Peter W. D.

TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
 ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: CLO00152

CURRENT APPLICATION NUMBER: US/60/187,217
 CURRENT FILING DATE: 1988-11-24
 NUMBER OF SEQ ID NOS: 23195

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9945
 LENGTH: 521
 TYPE: PRT

ORGANISM: Drosophila
 US-60-187-217-9945

Query Match 82.1%; Score 32; DB 24; Length 521;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYSSSNV 8
 Db 510 SYDANV 517

RESULT 13
 US-60-191-637-9950
 Sequence 9950, Application US/60191637
 GENERAL INFORMATION:
 APPLICANT: Ventner, J. Craig

TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
 GENES EXPRESSED FROM THE DROSOPHILA GENOME, AND
 TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: CLO00392

CURRENT APPLICATION NUMBER: US/60/191,637
 CURRENT FILING DATE: 1998-11-23
 NUMBER OF SEQ ID NOS: 12660

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9950
 LENGTH: 521
 TYPE: PRT

ORGANISM: DROSOPHILA
 US-60-191-637-9950

Query Match 82.1%; Score 32; DB 24; Length 521;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYSSSNV 8
 Db 510 SYDANV 517

RESULT 14
 US-60-173-464-1878
 Sequence 1878, Application US/60173464


```

: GENERAL INFORMATION:
: APPLICANT: Li, Peter W.D.
: TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
: FILE REFERENCE: C1000173
: CURRENT APPLICATION NUMBER: US/60/173,464
: CURRENT FILING DATE: 1999-12-29
: NUMBER OF SEQ ID NOS: 30269
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1878
: LENGTH: 542
: TYPE: PRT
: ORGANISM: Drosophila
US-60-173-464-1878

```

```

Query Match      82.1% Score 32; DB 24; Length 542;
Best Local Similarity 85.7% Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYSSNV 7
       :|||||
Db      95 NYSSNV 101

```

```

RESULT 15
US-60-191-637-2271
: Sequence 2271, Application US/60191637
: GENERAL INFORMATION:
: APPLICANT: Venter, J. Craig
: TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
: TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
: TITLE OF INVENTION: GSSS THEREOF
: FILE REFERENCE: C1000173
: CURRENT APPLICATION NUMBER: US/60/191,637
: CURRENT FILING DATE: 2000-03-23
: NUMBER OF SEQ ID NOS: 42660
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 2271
: LENGTH: 542
: TYPE: PRT
: ORGANISM: DROSOPHILA
US-60-191-637-2271

```

```

Query Match      82.1% Score 32; DB 24; Length 542;
Best Local Similarity 85.7% Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SYSSNV 7
       :|||||
Db      95 NYSSNV 101

```

Search completed: November 19, 2001, 08:23:17
 Job time: 730 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2001, 08:23:32 ; Search time 11.44 Seconds

(without alignments)
3.725 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 SYDSNMV 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 25229 seqs, 5326477 residues

Total number of hits satisfying chosen parameters: 25229

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Labeling first 45 summaries

Database : Pending-Patents_AA_New:*

1: /cgn2_6/p/odata1/1/pa/US06_NEW_COMB.pep:*

2: /cgn2_6/p/odata1/1/pa/US06_NEW_COMB.pep:*

3: /cgn2_6/p/odata1/1/pa/US07_NEW_COMB.pep:*

4: /cgn2_6/p/odata1/1/pa/US07_NEW_COMB.pep:*

5: /cgn2_6/p/odata1/1/pa/US09_NEW_COMB.pep:*

6: /cgn2_6/p/odata1/1/pa/US09_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	10	5	US-09-972-656-23
2	31	79.5	10	5	US-09-972-656-130
3	31	79.5	10	5	US-09-972-656-130
4	31	79.5	10	5	US-09-972-656-130
5	31	79.5	10	5	US-09-972-656-130
6	31	79.5	10	5	US-09-972-656-130
7	31	79.5	10	5	US-09-972-656-130
8	31	79.5	10	5	US-09-972-656-130
9	31	79.5	10	5	US-09-972-656-130
10	31	79.5	10	5	US-09-972-656-130
11	31	79.5	10	5	US-09-972-656-130
12	31	79.5	10	5	US-09-972-656-130
13	31	79.5	10	5	US-09-972-656-130
14	31	79.5	10	5	US-09-972-656-130
15	31	79.5	10	5	US-09-972-656-130
16	31	79.5	10	5	US-09-972-656-130
17	31	79.5	10	5	US-09-972-656-130
18	31	79.5	10	5	US-09-972-656-130
19	31	79.5	10	5	US-09-972-656-130
20	31	79.5	10	5	US-09-972-656-130
21	31	79.5	10	5	US-09-972-656-130
22	31	79.5	10	5	US-09-972-656-130
23	31	79.5	10	5	US-09-972-656-130
24	31	79.5	10	5	US-09-972-656-130
25	31	79.5	10	5	US-09-972-656-130
26	31	79.5	10	5	US-09-972-656-130

28	26	66.7	396	5	US-09-815-242-11791	Sequence 11791, A
29	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
30	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
31	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
32	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
33	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
34	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
35	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
36	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
37	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
38	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
39	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
40	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
41	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
42	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
43	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
44	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A
45	26	66.7	804	5	US-09-815-242-11821	Sequence 11821, A

ALIGNMENTS

```

RESULT 1
US-09-972-656-23
Sequence 130, App1
APPLICANT: Tsai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 10
TYPE: PPT
ORGANISM: Homo sapiens
US-09-972-656-23

Query Match 79.5%; Score 31; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 SYDSNMV 7

RESULT 2
US-09-972-656-130
Sequence 130, Application US/09972656
APPLICANT: Tsai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 130
LENGTH: 103
TYPE: PPT
ORGANISM: Homo sapiens
FEATURES: Misc
LOCATION: (77)-(77)
OTHER INFORMATION: Unidentified

```

NAME/KEY: Misc.
 LOCATION: (33)..(33)
 OTHER INFORMATION: Unidentified
 NAME/KEY: Misc. (34)
 LOCATION: (33)..(34)
 OTHER INFORMATION: Unidentified
 NAME/KEY: Misc. (35)
 LOCATION: (35)..(35)
 OTHER INFORMATION: Unidentified
 NAME/KEY: Misc. (36)
 LOCATION: (36)..(36)
 OTHER INFORMATION: Unidentified
 US-09-972-656-130

Query Match
 Best Local Similarity 79.5%; Score 31; DB 5; Length 103;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDSSN 6
 DB 98 SYDSSN 103

RESULT 3
 US-09-972-656-88
 Sequence 88: Application US/09972656
 GENERAL INFORMATION:
 APPLICANT: Deshpande, Rajendra
 APPLICANT: Tsai, Mei-Mei
 TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
 REFERENCE: 73-99
 CURRENT FILING DATE: 2001-10-05
 NUMBER OF SEQ ID NOS: 135
 SOFTWARE: Patent version 3.0
 SEQ ID NO 88
 LENGTH: 217
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-972-656-88

Query Match
 Best Local Similarity 79.5%; Score 31; DB 5; Length 217;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDSSN 6
 DB 93 SYDSSN 98

RESULT 4
 US-09-915-242-10393
 Sequence 10393: Application US/09815242
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Karl L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELTRA-011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIORITY FILING DATE: 2000-03-21
 PRIORITY FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: 60/269,308
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10393
 LENGTH: 804
 TYPE: PRT
 ORGANISM: Escherichia coli
 US-09-815-242-10393

Query Match
 Best Local Similarity 74.4%; Score 29; DB 5; Length 804;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDSSN 7
 DB 4 SYDSSN 10

RESULT 5
 US-09-815-242-13920
 Sequence 13920: Application US/09815242
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Karl L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELTRA-011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/219,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 13920
 LENGTH: 804
 TYPE: PRT
 ORGANISM: Salmonella typhi
 US-09-815-242-13920

Query Match
 Best Local Similarity 74.4%; Score 29; DB 5; Length 804;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 SYDSNRY 7
        ||||||:
        4 SYDSST 10

RESULT 6
US-09-972-656-31
: SEQUENCE 133: Application US/09972656
: GENERAL INFORMATION:
: APPLICANT: Deshpande, Rajendra
: APPLICANT: Tsai, Mei-Mei
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: FILE REFERENCE: A999 Neutralizing Activity
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 31
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-972-656-31

Query Match
Best Local Similarity 71.8%; Score 28; DB 5; Length 11;
                        83.3%; Pred. No. 0.64;
Matches 5: Conservative 1; Mismatches 0; Gaps 0;

OY      1 SYDSNRY 6
        ||||||:
        2 SYDSNRY 7

RESULT 7
US-09-972-656-102
: SEQUENCE 102: Application US/09972656
: GENERAL INFORMATION:
: APPLICANT: Deshpande, Rajendra
: APPLICANT: Tsai, Mei-Mei
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: FILE REFERENCE: A999 Neutralizing Activity
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 102
: LENGTH: 218
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-972-656-102

Query Match
Best Local Similarity 71.8%; Score 28; DB 5; Length 218;
                        83.3%; Pred. No. 10;
Matches 5: Conservative 1; Mismatches 0; Gaps 0;

OY      1 SYDSNRY 6
        ||||||:
        93 SYDSNRY 98

RESULT 8
US-09-986-055-445
: SEQUENCE 445: Application US/0986055
: GENERAL INFORMATION:
: APPLICANT: STRAYER, LUBERT
: APPLICANT: ZOZULYA, SERGEY
: TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
: FILE REFERENCE: A999 BIOSENSORS OF CHEMICAL SENSANTS
: CURRENT FILING DATE: 2000-07-23
: PRIOR APPLICATION NUMBER: US/09/886,055

CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
INVENTOR: ZOZULYA, SERGEY
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 445
LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-055-445

Query Match
Best Local Similarity 71.8%; Score 28; DB 5; Length 315;
                        62.5%; Pred. No. 24;
Matches 5: Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      1 SYDSNRY 8
        ||||||:
        167 SYDSNRY 174

RESULT 9
US-09-886-055-133
: SEQUENCE 133: Application US/0986055
: GENERAL INFORMATION:
: APPLICANT: STRAYER, LUBERT
: APPLICANT: ZOZULYA, SERGEY
: TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
: FILE REFERENCE: 078003-0277150
: CURRENT APPLICATION NUMBER: 09/09/886,055
: CURRENT FILING DATE: 2000-06-22
: PRIOR APPLICATION NUMBER: 60/213,812
: PRIOR FILING DATE: 2000-06-22
: NUMBER OF SEQ ID NOS: 522
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 133
: LENGTH: 316
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-886-055-133

Query Match
Best Local Similarity 71.8%; Score 28; DB 5; Length 316;
                        62.5%; Pred. No. 24;
Matches 5: Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      1 SYDSNRY 8
        ||||||:
        167 SYCSNRY 174

RESULT 10
US-09-815-242-14039
: SEQUENCE 14039: Application US/09815242
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlson, Karl L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel D.
: APPLICANT: Grant, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELTRA 011A US/09/815,242
: CURRENT APPLICATION NUMBER: 09/01-21
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/705,848
: PRIOR FILING DATE: 2000-05-23
```

```

? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 1410
? SOFTWARE: PASTED FOR Windows Version 4.0
? SEQ ID NO: 14039
? LENGTH: 350
? TYPE: PRT
? ORGANISM: Salmonella typhi
US-09-815-242-14039

```

```

Query Match
Best Local Similarity 71.8% Score 28; DB 5; Length 350;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SYDSNVS 7
DB 126 SFDASNV 132

```

```

RESULT 11
US-09-815-242-5222
? SEQUENCE: 1222, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Olsen, Karl L.
? APPLICANT: Zyckind, Judith W.
? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John D.
? APPLICANT: Yano, Grant J.
? APPLICANT: Yano, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? FILE REFERENCE: ELITRA.011A
? CURRENT APPLICATION NUMBER: US/09/815,242
? PRIOR APPLICATION NUMBER: 2001-03-21
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 1410
? SOFTWARE: PASTED FOR Windows Version 4.0
? SEQ ID NO: 5222
? LENGTH: 638
? TYPE: PRT
? ORGANISM: Staphylococcus aureus
US-09-815-242-5222

```

```

Query Match
Best Local Similarity 71.8% Score 28; DB 5; Length 638;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SYDSNVS 7

```

```

DB 54 NIDSQNV 60

```

```

RESULT 12
US-09-815-242-12143
? SEQUENCE: 12143, Application US/09815242
? GENERAL INFORMATION:
? APPLICANT: Haselbeck, Robert
? APPLICANT: Olsen, Karl L.
? APPLICANT: Zyckind, Judith W.
? APPLICANT: Wall, Daniel
? APPLICANT: Trawick, John D.
? APPLICANT: Yano, Grant J.
? APPLICANT: Yano, Robert T.
? APPLICANT: Xu, H. Howard
? TITLE OF INVENTION: Identification of Essential Genes in
? FILE REFERENCE: ELITRA.011A
? CURRENT APPLICATION NUMBER: US/09/815,242
? PRIOR APPLICATION NUMBER: 2001-03-21
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/191,078
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/206,848
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/207,727
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: 60/242,578
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: 60/253,625
? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 1410
? SOFTWARE: PASTED FOR Windows Version 4.0
? SEQ ID NO: 12143
? LENGTH: 642
? TYPE: PRT
? ORGANISM: Staphylococcus aureus
US-09-815-242-12143

```

```

Query Match
Best Local Similarity 71.8% Score 28; DB 5; Length 642;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SYDSNVS 7

```

```

DB 54 NIDSQNV 60

```

```

RESULT 13
US-09-978-249-8
? SEQUENCE: 8, Application US/09978249
? GENERAL INFORMATION:
? APPLICANT: Peterson, et al.
? FILE REFERENCE: Extracellular Matrix Polynucleotides, Polypeptides, and Antibio
? CURRENT APPLICATION NUMBER: US/09/978,249
? PRIOR APPLICATION NUMBER: PCT/US01/11643
? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: 60/198,123
? PRIOR FILING DATE: 2000-04-18
? NUMBER OF SEQ ID NOS: 16
? SOFTWARE: Patent Ver. 2.0
? SEQ ID NO: 8
? LENGTH: 798
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-978-249-8

```

Query Match 71.8%; Score 28; DB 5; Length 798;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Search completed: November 19, 2001, 08:23:32
 Job time: 744 sec

OY 1 SYDSNV 8
 DB 360 SMOSSNVL 367

RESULT 14
 US-09-972-656-48
 : Sequence 48, Application US/09972656
 : GENERAL INFORMATION:
 : APPLICANT: Deshpande, Rajendra
 : APPLICANT: Tsai, Mei-Mei
 : APPLICANT: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
 : TITLE OF INVENTION: Neutralizing Activity
 : FILE REFERENCE: A-799
 : CURRENT FILING DATE: 2001-10-05
 : CURRENT FILING DATE: 2001-10-05
 : NUMBER OF SEQ ID NOS: 135
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 48
 : LENGTH: 1
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-972-656-48

Query Match 69.2%; Score 27; DB 5; Length 17;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SYDSN 6
 DB 3 SYDSN 8

RESULT 15
 US-09-453-234-102
 : Sequence 102, Application US/09453234
 : GENERAL INFORMATION:
 : APPLICANT: Buechler, Joe
 : APPLICANT: Walkers, Gunars
 : APPLICANT: Gray, Jeff
 : APPLICANT: Lomborg, Nils
 : APPLICANT: Biosite Diagnostics, Inc.
 : APPLICANT: Biosite Diagnostics, Inc.
 : TITLE OF INVENTION: Human Antibodies
 : FILE REFERENCE: 020015-00011005
 : CURRENT APPLICATION NUMBER: US/09/453, 234
 : CURRENT FILING DATE: 1999-12-01
 : PRIOR FILING DATE: 1999-10-02
 : NUMBER OF SEQ ID NOS: 112
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 102
 : LENGTH: 225
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : OTHER INFORMATION: M2-31H
 US-09-453-234-102

Query Match 69.2%; Score 27; DB 5; Length 225;
 Best Local Similarity 83.3%; Pred. No. 27;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SYDSN 6
 DB 52 SYDSN 57

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: November 19, 2001, 08:13:26 ; Search time 43.5 Seconds

(without alignments)
4,135 Million cell updates/sec

Title: US-09-610-118-66

Perfect score: 39

Sequence: 1 STYSSNNV 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued-Patents.AA:*
2: /cgn2.6/pdata/2/1aa/5A.COMB.pep:*
3: /cgn2.6/pdata/2/1aa/2B.COMB.pep:*
4: /cgn2.6/pdata/2/1aa/5B.COMB.pep:*
5: /cgn2.6/pdata/2/1aa/PCPUS.COMB.pep:*
6: /cgn2.6/pdata/2/1aa/Backfiles1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	222	US-07-869-933-12	Sequence 12, Appl
2	31	79.5	222	US-07-869-933-12	Sequence 12, Appl
3	31	79.5	222	US-09-103-663-12	Sequence 12, Appl
4	31	79.5	222	US-09-103-663-12	Sequence 28, Appl
5	30	76.9	252	PCT-US96-01314-58	Sequence 58, Appl
6	30	76.9	253	PCT-US96-01314-58	Sequence 53, Appl
7	30	76.9	618	US-08-961-083-72	Sequence 72, Appl
8	30	76.9	618	US-08-961-083-72	Sequence 10, Appl
9	30	76.9	676	US-08-530-112-10	Sequence 10, Appl
10	30	76.9	676	US-08-769-078-10	Sequence 10, Appl
11	30	76.9	769	US-08-762-633-1	Sequence 1, Appl
12	30	76.9	769	US-08-476-62A-45	Sequence 1, Appl
13	30	76.9	769	US-07-728-215-31	Sequence 31, Appl
14	30	76.9	769	PCT-US95-04886-1	Sequence 45, Appl
15	30	76.9	769	PCT-US95-01314-45	Sequence 45, Appl
16	30	76.9	769	US-08-931-358E-152	Sequence 15, Appl
17	29	74.4	25	US-08-378-761A-30	Sequence 30, Appl
18	29	74.4	25	US-08-485-286-30	Patent No. 5248606
19	29	74.4	25	US-08-679-405-6	Sequence 6, Appl
20	29	74.4	40	US-08-842-799-6	Sequence 6, Appl
21	29	74.4	40	PCT-US96-11458-6	Sequence 6, Appl
22	29	74.4	160	PCT-US96-11458-6	Sequence 3, Appl
23	29	74.4	469	US-08-378-313-33	Sequence 3, Appl
24	29	74.4	600	US-08-679-405-2	Sequence 2, Appl
25	29	74.4	600	US-08-842-799-2	Sequence 2, Appl
26	29	74.4	600	US-09-271-778-2	Sequence 2, Appl
27	29	74.4	600	US-09-271-778-2	Sequence 2, Appl

ALIGNMENTS

28	29	74.4	600	5	PCT-US96-11458-2	Sequence 2, Appl
29	29	74.4	40	2	US-08-410-784A-4	Sequence 4, Appl
30	29	74.4	818	4	US-09-346-297A-1	Sequence 1, Appl
31	29	74.4	818	4	US-09-346-297A-1	Sequence 2, Appl
32	28	71.8	18	1	US-07-800-364B-2	Sequence 2, Appl
33	28	71.8	18	5	PCT-US91-03388-8	Sequence 8, Appl
34	28	71.8	49	1	US-07-800-364B-8	Sequence 8, Appl
35	28	71.8	49	5	PCT-US91-03388-8	Sequence 1, Appl
36	28	71.8	102	3	US-08-478-097A-17	Sequence 17, Appl
37	28	71.8	102	3	US-08-931-358E-152	Sequence 15, Appl
38	28	71.8	102	4	US-08-931-358E-152	Sequence 15, Appl
39	28	71.8	112	1	US-07-800-364B-12	Sequence 12, Appl
40	28	71.8	112	5	PCT-US91-03388-13	Sequence 13, Appl
41	28	71.8	119	4	US-08-624-635-15	Sequence 15, Appl
42	28	71.8	139	1	US-08-278-729A-7	Sequence 7, Appl
43	28	71.8	139	1	US-08-278-729A-6	Sequence 7, Appl
44	28	71.8	139	1	US-08-135-343A-7	Sequence 7, Appl
45	28	71.8	139	1	US-08-135-343A-6	Sequence 8, Appl

RESULT 1
US-07-869-933-12
Sequence 12, Application US/07869933
Patent No. 5270356
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
ADDRESS: POLYMERLANDER
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0259
COMPUTER: IBM PC COMPATIBLE
MEDIUM TYPE: 3.5 inch disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 1992/04/16
CLASSIFICATION: C12N 1/21
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHID
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/936-9300
FAX: 703/936-9300
TELEX: 899149
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULAR TYPE: protein
ORGANISM: SOURCE: rat
STRAIN: PCRI alpha subunit
US-07-869-933-12

Query Match 79.5% Score 31, DB 1, Length 222:
Local Similarity 73.4%
Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:

QY 1 SYSSNV 7
 Db 130 SYSSNMI 136

RESULT 2
 US-07-669-933-28
 Sequence 28, Application US/07869933
 Patent No. 5770396
 GENERAL INFORMATION:
 APPLICANT: KINET, Jean-Pierre
 TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
 THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
 IMMUNOGLOBULIN E.
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.25
 CURRENT FILING DATE: 1998-06-23
 EARLIER FILING DATE: 19920416
 FILING DATE: 19920416
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,766
 REFERENCE/DOCKET NUMBER: 40399/154 NTHD
 TELEPHONE: (703)836-9300
 TELEFAX: (703)836-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 222 amino acids
 TOPOLOGY: 1
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 STRAIN: alpha subunit
 US-07-669-933-28

Query Match 79.5% Score 31; Db 1; Length 222;
 Best Local Similarity 71.4% Pred. No. 56;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYSSNV 7
 Db 130 SYSSNMI 136

RESULT 3
 US-09-103-663-12
 Sequence 12, Application US/09103663D
 Patent No. 6171803
 GENERAL INFORMATION:
 APPLICANT: KINET, et al.
 TITLE OF INVENTION: Isolation, characterization, and use of the human beta
 subunit of the high affinity receptor for
 FILE REFERENCE: 50490
 CURRENT APPLICATION NUMBER: US/09/103,663D
 CURRENT FILING DATE: 1998-06-23
 EARLIER APPLICATION NUMBER: 07/869,933
 EARLIER FILING DATE: 1992-04-16

; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 222
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-103-663-12

Query Match 79.5% Score 31; Db 4; Length 222;
 Best Local Similarity 71.4% Pred. No. 56;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYSSNV 7
 Db 130 SYSSNMI 136

RESULT 4
 US-09-103-663-28
 Sequence 28, Application US/09103663D
 Patent No. 6171803
 GENERAL INFORMATION:
 APPLICANT: Kinet et al.
 TITLE OF INVENTION: Isolation, characterization, and use of the human beta
 subunit of the high affinity receptor for
 FILE REFERENCE: 50490
 CURRENT APPLICATION NUMBER: US/09/103,663D
 CURRENT FILING DATE: 1998-06-23
 EARLIER FILING DATE: 1992-04-16
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 28
 LENGTH: 222
 TOPOLOGY: 1
 ORGANISM: Homo sapiens
 US-09-103-663-28

Query Match 79.5% Score 31; Db 4; Length 222;
 Best Local Similarity 71.4% Pred. No. 56;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYSSNV 7
 Db 130 SYSSNMI 136

RESULT 5
 US-06-01314-58
 Sequence 58, Application PC/TUS9601314
 GENERAL INFORMATION:
 APPLICANT: M. Amlin Arnaut
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: F. H. Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 COMPUTER: IBM PS/2 Model 50Z or 555X
 OPERATING SYSTEM: MS-DOS (version 5.0)
 SOFTWARE: WordPerfect (version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/01314
 FILING DATE: 30-JAN-96

Prior APPLICATION DATA:
 APPLICATION NUMBER: 08/380,167
 FILING DATE: 30-JAN-95
 ATTORNEY/AGENT INFORMATION:
 NAME: John W. Freeman
 REGISTRATION NUMBER: 29, 066
 REFERENCE/DOCKET NUMBER: 00786/267001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8908
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 252 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-01314-58

Query Match 76.9%; Score 30; DB 5; Length 252;
 Best Local Similarity 87.5%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1;

Qy 1 SYSDSNV 8
 Db 237 SYSDSNV 244

RESULT 6
 PCT-US96-01314-53
 Sequence 53, Application FC/TUS9601314
 GENERAL INFORMATION:
 APPLICANT: M. Amin Arnaout
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS: 1450
 ADDRESS: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/01314
 FILING DATE: 30-JAN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/380,167
 FILING DATE: 30-JAN-95
 ATTORNEY/AGENT INFORMATION:
 NAME: John W. Freeman
 REGISTRATION NUMBER: 29, 066
 REFERENCE/DOCKET NUMBER: 00786/267001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8908
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-01314-53

Query Match 76.9%; Score 30; DB 5; Length 253;
 Best Local Similarity 87.5%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1;

Qy 1 SYSDSNV 8
 Db 238 SYSDSNV 245

RESULT 7
 US-08-961-083-72
 Sequence 72, Application US/08961083
 Patent No. 6199469
 GENERAL INFORMATION:
 APPLICANT: Choi et. al.
 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
 NUMBER OF SEQUENCES: 432
 CORRESPONDENCE ADDRESS: 432
 ADDRESS: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
 OPERATING SYSTEM: HP Vectra 486/33
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/961,083
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 36,173
 REFERENCE/DOCKET NUMBER: 36,173/4092
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 618 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-961-083-72

Query Match 76.9%; Score 30; DB 4; Length 618;
 Best Local Similarity 73.0%; Pred. No. 2.7e+02; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1;

Qy 1 SYSDSNV 8
 Db 363 SYSDSNV 370

RESULT 8
 US-08-630-172-10
 Sequence 10, Application US/08630172
 Patent No. 6060054
 GENERAL INFORMATION:
 APPLICANT: Staetz, Uwe
 TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:

ADDRESS: Sheridan Ross & McIntosh
 STREET: 1700 Lincoln Street, 35th Floor
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/630,172
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2879-36
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 676 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-630-172-10

Query Match 76.9% Score 30; DB 3; Length 676;
 Best Local Similarity 87.5% Pred. No. 3e+02; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1;
 Oy 1 SSSSNV 8
 Db 324 SSSSNV 331

RESUM 9
 US-08-375-419-10
 Sequence 10 Application US/09375419
 Patent No. 6264950
 GENERAL INFORMATION:
 APPLICANT: Steerz, Uwe
 TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESS: Sheridan Ross & McIntosh
 STREET: 1700 Lincoln Street, 35th Floor
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/375,419
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/630,172
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2879-36
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 676 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-375-419-10

Query Match 76.9% Score 30; DB 4; Length 676;
 Best Local Similarity 87.5% Pred. No. 3e+02; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1;
 Oy 1 SSSSNV 8
 Db 324 SSSSNV 331

RESUM 10
 US-08-789-078-1
 Sequence 1 Application US/08789078
 Patent No. 5843885
 GENERAL INFORMATION:
 APPLICANT: Benedict, Stephen H.
 APPLICANT: Slabaugh, Teruna
 APPLICANT: Chen, Marcia
 TITLE OF INVENTION: ICAM-1/ICAM-1/ICAM-1 PEPTIDES FOR INDUCING
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESS: HOVEY, WILLIAMS, TIMMONS & COLLINS
 STREET: 1101 Walnut St.
 CITY: Kansas City
 STATE: Kansas
 COUNTRY: USA
 ZIP: 64108
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/789,078
 FILING DATE: 03-FEB-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/229,513
 FILING DATE: 08-22-94
 ATTORNEY/AGENT INFORMATION:
 NAME: Collins, John M.
 REGISTRATION NUMBER: 26262
 REFERENCE/DOCKET NUMBER: 22833
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816)474-9050
 TELEFAX: (816)474-9057
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 769 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 MOLECULE TYPE: protein
 HYDROTHERMAL: NO
 ORGANOLOGICAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: Tonsil
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..22
 OTHER INFORMATION: /label= signal

OTHER INFORMATION: /note= "signal sequence"
FEATURE: Region
NAME/KEY: Region
LOCATION: 449..496
OTHER INFORMATION: /label= repeat
OTHER INFORMATION: /note= "cysteine rich repeat"
FEATURE:
NAME/KEY: Region
LOCATION: 497..540
OTHER INFORMATION: /label= repeat
OTHER INFORMATION: /note= "cysteine rich repeat"
FEATURE: Region
NAME/KEY: Region
LOCATION: 541..581
OTHER INFORMATION: /label= repeat
OTHER INFORMATION: /note= "cysteine rich repeat"
FEATURE: Region
NAME/KEY: Region
LOCATION: 582..617
OTHER INFORMATION: /label= repeat
OTHER INFORMATION: /note= "cysteine rich repeat"
FEATURE:
NAME/KEY: Domain
LOCATION: 701..723
OTHER INFORMATION: /label= trans
OTHER INFORMATION: /note= "transmembrane domain"
FEATURE: Domain
NAME/KEY: Domain
LOCATION: 724..769
OTHER INFORMATION: /label= cyto
OTHER INFORMATION: /note= "cytoplasmic domain"
PUBLICATION INFORMATION:
AUTHORS: Pigott,
TITLE: LFA-1 Amino acid sequence (B2) (from human
JOURNAL: The Adhesion Molecule Facts Book
PAGES: 96-96
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 769
US-08-752-633-1
Query Match 76.9%; Score 30; DB 2; Length 769;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 1 SYSSNVV 8
DB 346 SEDSSNVV 353

RESULT 11
US-08-752-633-1
Sequence 1, Application US/08/52633
Accession 52633
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Sibaah, Teruna
APPLICANT: Tibbels, Scott
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
CELL-CELL ADHESION: IMMUNE TOLERANCE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
COUNTRY: USA
APPLICATION NUMBER: US/08/752,633
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELEPHONE: (816)474-9050
TELEFAX: (816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Tonsil
FEATURE: Region
NAME/KEY: Region
LOCATION: 1..22
OTHER INFORMATION: /label= signal
OTHER INFORMATION: /note= "signal sequence"
FEATURE:
NAME/KEY: Region
LOCATION: 449..496
OTHER INFORMATION: /label= repeat
OTHER INFORMATION: /note= "cysteine rich repeat"
FEATURE:
NAME/KEY: Region
LOCATION: 497..540
OTHER INFORMATION: /label= repeat
OTHER INFORMATION: /note= "cysteine rich repeat"
FEATURE: Region
NAME/KEY: Region
LOCATION: 541..581
OTHER INFORMATION: /label= repeat
OTHER INFORMATION: /note= "cysteine rich repeat"
FEATURE:
NAME/KEY: Region
LOCATION: 582..617
OTHER INFORMATION: /label= repeat
OTHER INFORMATION: /note= "cysteine rich repeat"
FEATURE:
NAME/KEY: Domain
LOCATION: 701..723
OTHER INFORMATION: /label= trans
OTHER INFORMATION: /note= "transmembrane domain"
FEATURE: Domain
NAME/KEY: Domain
LOCATION: 724..769
OTHER INFORMATION: /label= cyto
OTHER INFORMATION: /note= "cytoplasmic domain"
PUBLICATION INFORMATION:
AUTHORS: Pigott,
TITLE: LFA-1 Amino acid sequence (B2) (from human
JOURNAL: The Adhesion Molecule Facts Book
PAGES: 96-96
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 769
US-08-752-633-1
Query Match 76.9%; Score 30; DB 2; Length 769;

Beat Local Similarity 87.5%: Pred. No. 3.4e+02:
Matches 7: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 SYOSSNV 8
DB 346 SSSSNV 353

RESULT 12
US-08-476-062A-45
Sequence 45, Application US/08476062A
PATENT No. 5877275
GENERAL INFORMATION:
APPLICANT: M. Arin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSES: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA 02110
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER SYSTEM: WINDOWS95
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/216,061
FILING DATE: 21-MAR-1994
PRIORITY NUMBER: 07/277,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1988
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 129,066
REFERENCE/DOCKET NUMBER: 00766/068003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200124
INSTRUMENT ID NO.: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
REAGENT TYPE: Internal
US-08-476-062A-45

Query Match 76.9%: Score 30: DB 2: Length 769:
Beat Local Similarity 87.5%: Pred. No. 3.4e+02:
Matches 7: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 SYOSSNV 8
DB 346 SSSSNV 353

RESULT 13
US-07-728-215-31
Sequence 31, Application US/07728215
PATENT No. 5962443
GENERAL INFORMATION:

APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pyrcela, Robert
TITLE OF INVENTION: A No. 59626343el Integrin Beta Subunit and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSES: Schrodter, Brueggemann & Clark
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" disk
COMPUTER SYSTEM: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/728,215
FILING DATE: 19910711
PRIORITY NUMBER: 07/215,311
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8845
INSTRUMENT ID NO.: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-728-215-31

Query Match 76.9%: Score 30: DB 2: Length 769:
Beat Local Similarity 87.5%: Pred. No. 3.4e+02:
Matches 7: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 SYOSSNV 8
DB 346 SSSSNV 353

RESULT 14
PCT-US95-04886-1
Sequence 1, Application PC/TUS9504886
GENERAL INFORMATION:
APPLICANT: Shannick, Stephen H.
APPLICANT: Shannick, Stephen H.
APPLICANT: Chan, Marcia
TITLE OF INVENTION: 10AM-1/LPA-1 PEPTIDES FOR INDUCING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSES: TIMMONS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER SYSTEM: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04886
FILING DATE:

```

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME/KEY: Region
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: (816)474-9050
INVENTOR: US 28 ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Tonsil
FEATURE:
NAME/KEY: Region
LOCATION: 1..22
OTHER INFORMATION: /label= signal
FEATURE:
NAME/KEY: Region
LOCATION: 443..496
OTHER INFORMATION: /note= cysteine rich repeat*
FEATURE:
NAME/KEY: Region
LOCATION: 582..617
OTHER INFORMATION: /label= repeat
FEATURE:
NAME/KEY: Region
LOCATION: 497..540
OTHER INFORMATION: /label= repeat
FEATURE:
NAME/KEY: Region
LOCATION: 541..581
OTHER INFORMATION: /note= cysteine rich repeat*
FEATURE:
NAME/KEY: Region
LOCATION: 582..617
OTHER INFORMATION: /label= repeat
FEATURE:
NAME/KEY: Domain
LOCATION: 701..723
OTHER INFORMATION: /label= trans
FEATURE:
NAME/KEY: Domain
LOCATION: 724..769
OTHER INFORMATION: /note= transmembrane domain*
FEATURE:
NAME/KEY: Domain
LOCATION: 724..769
OTHER INFORMATION: /note= cytoplasmic domain*
PUBLICATION INFORMATION:
AUTHORS: Power,
TITLE: LFA-1 amino acid sequence (B2) (from human
JOURNAL: The Adhesion Molecule Facts Book
PAGES: 96-96
DATE: 1992
PCT-US95-04886-1
PCT-US95-04886-1

```

```

Query Match 76.9%; Score 30; DB 5; Length 769;
Best Local Similarity 87.5%; Pred. NO. 3.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 SYDSNNV 8
DB 346 SEDSSNV 353

```

```

RESULT 15
PCT-US96-01314-45
Sequence 45, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
NUMBER OF SEQUENCES: 78
ADDRESS: Fish & Richardson P.C.
CITY: Boston
STREET: 225 Franklin Street
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
INVENTOR: M. Amin Arnaout, 144 MB
OPERATING SYSTEM: IBM PS/2 Model 502 or 555X
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIORITY INFORMATION:
PRIORITY INFORMATION: 08/280,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 769
TYPE: amino acid
SYDSNNV: 8
TOPOLOGY: linear
PCT-US96-01314-45

```

```

Query Match 76.9%; Score 30; DB 5; Length 769;
Best Local Similarity 87.5%; Pred. NO. 3.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 SYDSNNV 8
DB 346 SEDSSNV 353
Search completed: November 19, 2001, 08:13:27
Job time: 140 sec

```

